



PATENT
Attorney Docket No. NREL 01-35:
Express Mail Label No. *712*

THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Ding et al.

Examiner: Manjunath Rao

Serial No. 09/917,378

Group Art Unit: 1652

Filed: July 28, 2001

Confirmation No. 9985

For: THERMAL TOLERANT
MANNANASE FROM
ACIDOTHERMUS
CELLULOLYTICUS

RECEIVED

MAY 0 2 2003

TECH CENTER 1600/2900

Box: FEE AMENDMENT
Commissioner for Patents
Washington, DC 20231

Sir:

DECLARATION OF SHI-YOU DING, Ph.D

37 C.F.R. §1.132

1. I am the Shi-You Ding who is named as an inventor in the above-identified application.
2. Exhibit A to this Declaration is my curriculum vitae. I am currently employed at the National Renewable Energy Laboratory in Golden, Colorado where I work as a Senior Research Scientist. I have many years of bench research experience in the field of microbiology with focus in hydrolyzing enzymes.
3. This declaration is provided with evidence that refutes certain of the Examiner's arguments in the Office Action dated January 10, 2003.
4. The first issue is to address the arguments beginning on page 7 and which concern the rejection of claims 1-5 and 12-13 because the specification allegedly does not enable claims this broad. For the reasons explained below, this cannot be the case where the claims identify well known families of domains.
5. Exhibit B to this Declaration contains an excerpt of information that is published in the CAZy database (cited as Coutinho, P.M. & Henrissat, B. (1999)

Carbohydrate-Active Enzymes server at URL: <http://afmb.cnrs-mrs.fr/~cazy/CAZY/index.html>). CAZy was produced over a ten year period and contains cross-linkages to a variety of international sequence databases. The "Family GH5" domains extend from pages 1 to 13 of Exhibit B. The Family CBDIII domains extend from pages 16 to 18. The "Family CBDII domains extend from pages 19-22.

6. Scientists who practice in my field are routinely trained in the use of computer databases, such as the CAZy, GenBank, and SwissProt databases identified in Exhibit B. The mere mention that a particular poly[peptide domain is classified in of one of these families causes an instant recognition that the domain is in a similar classification with respect to other domains in that family. The ability to access domains by this classification system is a fundamental and basic part of our working knowledge.

7. Therefore, it is simply not correct for the Examiner to say that the specification fails to disclose the multiple modifications encompassed by the instant claims. Multiple modifications are, in fact, disclosed by the domain family names. Those skilled in the art appreciate from the disclosure in the specification that these well known family domains may be linked together in perhaps thousands of permutations of GH5-CBDIII-CBDII domains. Furthermore, molecular genetics are sufficiently advanced that those following the disclosure of the present specification would routinely be able to make such linkages.

8. It follows that the allegations raised as points A through E in the passage bridging pages 8-9 are false. The specification does disclose a specific guidance and rationale for practicing the claimed invention when it refers to the domain family names.

9. Another issue is that on page 15 of the Office Action the Examiner has shifted the burden to Applicants to prove that Gibbs et al., Appl. Environ. Microbiol. 58(12) 3864-3867 (1992) does not contain linked GH5-CBHIII-CBHII domains.

10. Exhibit C to this Declaration is an excerpt from the Swiss Prot database, and it contains a summary of the sequence reported by Gibbs. The middle portion of page 2 thereof contains a summary of the domains.

11. I have studied Exhibit C to classify the domains identified on page 2 thereof. Handwritten comments of "GH5," "CBDII," and "CBDII" indicate my conclusion that Gibbs teaches a sequence of GH5-CBDII-CBDII family domains. This is not the sequence of GH5-CBDIII-CBDII that is presently recited in claim 1.

12. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like are punishable by fine or imprisonment, or both, under 18 U.S.C. § 1001, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: 4-22-03

By: Shi-You Ding

Shi-You Ding, Ph.D

SHI-YOU DING *Ph.D*

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EDUCATION

Postdoctoral fellow , The Weizmann Institute of Science & Tel Aviv University, Israel	1997-2000
Ph.D , Peking University & The Chinese Academy of Sciences, China	1994
M.S. The Chinese Academy of Sciences, China	1989
B.Sc. Anhui Normal University, China	1986

MEMBERSHIPS

American Society of Microbiology, American Chemical Society

PROFESSIONAL EXPERIENCE

Scientist II , National Renewable Energy Laboratory	2002-present
Research associate , National Renewable Energy Laboratory	2000-2001

Nanotechnology. Understanding Nanoscale Chemistry: Quantum Dot Interactions with Proteins and Carbon Nanotubes and the Mediation of Inter-Quantum Dot Communication.

- ❖ Cloned and expressed clostridia cellulosomal scaffoldin proteins
- ❖ Making protein/quantum dot conjugates
- ❖ Making quantum dots arrays by scaffoldin protein templates.

Cellulase Fundamentals. Biochemistry and molecular biology of enzyme system of cellulytic organism

- ❖ Cloned, sequenced four Glycoside Hydrolase genes from *Acidothermus cellulolyticus*. Four ROIs have been filed.
- ❖ Developed *E. coli* system for *Acidothermus* enzyme expression. Six catalytic domain of *Acidothermus* enzymes have been expressed and purified.
- ❖ Set up sequence database of CBHs (Family 7 cellulase), aligned the sequences of all available Family 7 cellulase, designed degenerate PCR primers for screening new CBHs from potential microorganisms.
- ❖ Assisted to identify new CBHs found from *Penicillium sp.* and other cellulose degraders, designed PCR primers for further gene cloning.

CBHI Expression. Evaluate the CBHI expression in different system, e.g. *E. coli*, fungi and insect cells.

- ❖ Cloned the catalytic domain of *T. reesei* CBHI into different expression vectors, including pET22b, pET32b, pET40b, pMAL-p2, generated ten CBHI-cd expression constructs, with or without signal sequences, fusion proteins, and tags.
- ❖ Expressed CBHI constructs in *E. coli* strains, including XL-1blue, BL21, BL21(DE3), BL21 *trx* (DE3), BL21(DE3)pLysS, Origami(DE3), Origami(DE3)pLysS, tested the expression level.
- ❖ Cloned CBHI-cd into a *E. coli* -fungi shuttle vector pPFE1 with or without 6xHis tag, prepared the constructs for expression CBHI-cd in fungi.

Co-PI proposals

- ❖ **DOE Office of Science National Nanotechnology Initiative:** Understanding Nanoscale Chemistry: Quantum Dot Interactions with Proteins and Carbon Nanotubes and the Mediation of Inter-Quantum Dot Communication. PI: Arthur J. Nozik
* This proposal has been funded at a level of \$750k/yr.
- ❖ **NASA OLMSA Microgravity Research Division:** Self-assembling Proteins: new Superlattice Structures for Efficient Electro-optic Devices. PI: Mike E. Himmel.
- ❖ **DOE Office of Science Microbial Cell Project:** Toward Understanding the Clostridial Cellulosome: A Bioinformatics Approach. PI: Mike E. Himmel.
- ❖ **DDRD:** Preparation and Characterization of Novel Quantum Dot/Protein Conjugates. PI: Mike E. Himmel & Garry Rumbles.

DOE Microbial Cell Project Review Panel (June 2001).

Postdoctoral fellow, The Weizmann Institute of Science & Tel Aviv University, Israel

1997-1999

- ❖ Identified high-molecular-weight (200-400 kDa) cellulosome-related proteins, including scaffolding proteins and cell surface anchoring proteins, from different cellulolytic bacteria.
- ❖ Constructed genomic libraries. Five genes encoding cellulosome-related protein, 6-12kb in size, were cloned from *Acetivibrio celiulolyticus*, *Bacteroides cellulosolvens*, and *Ruminococcus flavefaciens* (collaborated with Dr. Harry J. Flint, Rowett Research Institute, UK), respectively.
- ❖ Expressed and purified three functional domains.
- ❖ Crystallized and determined the crystal structure of CBD from *Clostridium cellulolyticum* scaffolding protein (collaborated with Dr. Linda Shimon et al. at The Weizmann Institute of Science).
- ❖ Crystallization of cohesin domains from *B. cellulosolvens*, *Ruminococcus flavefaciens*, and co-crystal of cohesin domain of scaffoldin and dockerin domain of catalytic subunit from *C. thermocellum* are still under processing.

Assistant Investigator, Peking University, China

1995-1996

- ❖ Cloning, and expression of plant resistance genes and molecular biology of Rice Dwarf Virus.
- ❖ DNA fragments isolation from ancient materials.
- ❖ Molecular evolution and systematics of Astragalinae.
- ❖ Constructed the local molecular biological database and the Homepage of the laboratory

Visiting Research Fellow, Peking University

1993-1994

- ❖ Molecular phylogenetic study on Astragalinae

Research Assistant, The Chinese Academy of Sciences

1989-1994

- ❖ Ecological investigation in wild field, specimen identification in herbarium
- ❖ Cladistic analysis of Astragalinae based on morphological and ultrastructural data.
- ❖ Ecological, floristic investigation of plants in Northern China.
- ❖ Microscopic and ultrastructural study on the anatomy of Staphyleaceae

GRANT & FELLOWSHIP

- ❖ **Co-PI (2000-2004): DOE Office of Science National Nanotechnology Initiative.** Understanding Nanoscale Chemistry: Quantum Dot Interactions with Proteins and Carbon Nanotubes and the Mediation of Inter-Quantum Dot Communication (PI: Arthur J. Nozik)
- ❖ **PI/co-PI (1991-1997): National Natural Science Foundation of China.**
PI: Molecular systematics of subtribe Astragalinae (Fabaceae),
Co-PI: Ancient DNA research (PI: Zhangliang Chen)
Co-PI: Systematics of Polygonatum (PI: Guangyun Rao)
- ❖ **PI/co-PI (1991-1995): other projects**
NLPGE Research Fellowships. PI: Phylogenetic Reconstruction of Subtribe Astragalinae: Evidence from Restriction Site Mapping of A PCR-amplified Fragment Which Encompassed cpDNA genes *ndhF* and *psbA*.
KIB Director Fellowships. PI: Systematics of Astragalinae

RECORD OF INVENTION

- ❖ Michael E. Himmel, **Shi-You. Ding**, Garry Rumbles and Arthur J. Nozik Generation of Ordered Arrays of Quantum Dots Using Cellulosome Protein Scaffolds. NREL New Invention No. 01-05.
- ❖ **Shi-You Ding**, William S. Adney, Todd B. Vinzant, Michael E. Himmel A Thermal Tolerant Avicelase from *Acidotherrnus cellulolyticus*. NREL Invention Disclosure #01-36, Filed 8/1/01
- ❖ William S. Adney, **Shi-You Ding**, Suzanne McCarter, Michael E. Himmel, Stephen R. Decker, and Todd B. Vinzant. A Thermal Tolerant Exoglucanase from *Acidotherrnus cellulolyticus*. NREL Invention Disclosure #01-38, Filed 8/1/01
- ❖ **Shi-You Ding**, William S. Adney, Todd B. Vinzant, Michael E. Himmel. A Thermal Tolerant Multi-Domain Cellulase from *Acidotherrnus cellulolyticus*. NREL Invention Disclosure #01-37, Filed 8/1/01
- ❖ **Shi-Y u Ding**, William S. Adney, Todd B. Vinzant, Michael E. Himmel. A Thermal Tolerant Mannanase from *Acidotherrnus cellulolyticus*. NREL Invention Disclosure #01-35, Filed 8/1/01

- ❖ Michael E. Himmel, Joshua Sakon, William S. Adney, Stephen R. Decker, Suzanne McCarter, **Shi-You Ding**, Todd B. Vinzant and John O. Baker. Site Specific Mutations Conferring Thermal Tolerance to *Trichoderma reesei* CBHI. NREL New Invention No. 01-31.

PUBLICATIONS

1. Xu, Q., Gao, W., **Ding, S.-Y.**, Kenig, R., Shoham, Y., Bayer, E. A., Lamed, R. 2003. A cellulosome-integrating gene cluster in *Acetivibrio cellulolyticus* contains a scaffoldin-like gene encoding for a novel type of adaptor protein. *J. Bacteriol.* (in press)
2. **Ding, S.-Y.**, Lamed, R., Bayer, E. A., Himmel, M. E. 2003. The bacterial scaffoldin: structure function and potential applications in the nanosciences. In *Genetic Engineering* (J. K. Setlow, ed.) Volume 25, Kluwer Academic/Plenum Publishers. (in press)
3. **Ding S.-Y.**, William S. Adney, Todd B. Vinzant Stephen R. Decker, John O. Baker, Steven R. Thomas, Michael E. Himmel. Glycosyl Hydrolases Gene Cluster of *Acidothermus cellulolyticus* ACS (in press)
4. Rincon M. T., **Ding, S.-Y.**, Mccrae S. I., Martin J. C., Aurilia V., Lamed R., Shoham Y., Bayer, E. A., Flint, H. J. 2003. Novel organization and divergent dockerin specificities in the cellulosome system of *Ruminococcus flavefaciens*. *J. Bacteriol.* 185:703-713.
5. William S. Adney, Yat-Chen Chou, Stephen R. Decker, **Ding, S.-Y.**, John O. Baker, Todd B. Vinzant, Glenn Kunkel, and Michael E. Himmel. Heterologous Expression of *Trichoderma reesei* 1,4-beta-D-glucan cellobiohydrolase. ACS (in press)
6. **Ding, S.-Y.**, Rincon M. T., Lamed R., Martin J. C., Mccrae S. I., Aurilia V., Shoham Y., Bayer, E. A., Flint, H. J. 2001. Cellulosomal Scaffoldin-Like Proteins from *Ruminococcus flavefaciens*. *J. Bacteriol.* 183:1945-1953.
7. **Ding, S.-Y.** Bayer, E. A., Steriner, D., Shoham, Y. and Lamed, R. 2000. An atypical scaffoldin of the *Bacteroides cellulosolvens* cellulosome that contains eleven type-II cohesins. *J. Bacteriol.* 182:4915-4925
8. Bayer, E. A., **Ding, S.-Y.**, Shoham, Y. and Lamed, R. New perspectives in the structure of cellulosome-related domains from different species. In *Genetics, biochemistry and ecology of cellulose degradation* (K. Ohmiya et al., ed.), 1999. pp. 428-436. Uni Publishers Co., Ltd., Tokyo, Japan.
9. **Ding, S.-Y.**, Bayer, E. A., Steriner, D., Shoham, Y. and Lamed, R. 1999. A Novel Cellulosomal Scaffoldin from *Acetivibrio cellulolyticus* That Contains a Family 9 Glycosyl Hydrolase. *J. Bacteriol.* 181:6720-6729.
10. Bayer, E. A., **Ding, S.-Y.**, Mechaly, A., Shoham, Y. and Lamed, R. 1999. Emerging phylogenetics of cellulosome structure, p. 189-201. In H. Gilbert, G. J. Davies, B. Henrissat, and B. Svensson (eds), *Recent advances in carbohydrate bioengineering*. The Royal Society of Chemistry, Cambridge.
11. **Ding, S.-Y.**, Gu, H., Qu, L., Chen, Z. A preliminary study on the use of RFLP analysis of the PCR amplified products in the systematic investigation of the subtribe Astragalinae (Fabaceae). *Acta Bot. Sin.* 1995, 7-102.
12. **Ding, S.-Y.**, Zhang, C., Gu, H., Chen, Z. Progresses of studies on plant systematics at DNA level. *Acta Bot. Boreal.-Occident. Sin.* 1996,16(3):578-588.
13. **Ding, S.-Y.**, Zhang, C., Gu, H., Chen, Z. General review of the methods of molecular systematics of plants at DNA level. *Acta Bot. Boreal.-Occident. Sin.* 1996,16(2): 197-202.
14. Chu, L., Li, Y., Quan, S., **Ding, S.-Y.**, Suzuki, R., Chen, Z. Sequence analysis and expression in *E. coli* of RDV S7. *Acta Microbiologica Sinica*, 1996,36(5):335-343.
15. **Ding, S.-Y.**, Zhang, C., Gu, H., Chen, Z. Plant systematics at DNA level, in *The Proceeding of the Symposium of the Postdoctor in China*. 1996, Pp. 938-943.
16. Chen, Y., Zhang, C., **Ding, S.-Y.**, Zhang, Z. The taxonomy and analysis of *Artemisia* Linn. In the Loess Plateau of northern Shaanxi. *Acta Bot. Boreal.-Occident. Sin.* 1993,13(3):238-245.
17. **Ding, S.-Y.**, Yu, Z. Systematic signification of leaf structure of Staphyleaceae. *Bull. Bot.* 1992,12(2):177-184.
18. **Ding, S.-Y.**, Yu, Z. The preliminary study on chemical taxonomy of Staphyleaceae. The 1st Symposium of Systematic Botany in Northwestern China. 1992,108-111.
19. Zhang, Z., Zhang, C., Chen, Y., **Ding, S.-Y.** A preliminary study in the border line of the floristic regionalization in the Loess Plateau of northern Shaanxi. *Acta Bot. Boreal.-Occident. Sin.* 1992,12(4):303.
20. Zhang, Y., **Ding, S.-Y.** A resource of nectariferous plants in Shaanxi. *Acta Bot. Boreal.-Occident. Sin.* 1991,185-189.
21. **Ding, S.-Y.**, Zhang, Y. The conservation plants in northwestern China, in *Ecological Environment in Northwestern China*. 1991,1:353-364.
22. Zhang, Z., Zhang, C., **Ding, S.-Y.** Plants in the Loess Plateau. In, *The Resource and Application of Plants in the Loess Plateau*. 1991,194-287.
23. **Ding, S.-Y.**, Yu, Z. Study on the pollen of Staphyleaceae. *Acta Bot. Boreal.-Occident. Sin.* 1988,8(5): 29-33.

Abstracts and presentations in international meetings

1. **Shi-You Ding**, Todd B. Vinzant, William S. Adney, Stephen R. Decker, John O. Baker, Ed Jennings, Michael E. Himmel New Glycosyl Hydrolases from *Acidothermus cellulolyticus* poster for 24th Symposium on Biotechnology For Fuels and Chemicals April 28 - May 1, 2002, Gatlinburg, TN
2. **S.-Y. Ding**, WS Adney, SE McCarter, JO Baker, SR Decker, TB Vinzant, ME Himmel. Diversity and Conservation of Relevant Glycoside Hydrolase Families in Well-studied Cellulolytic Microbes. Proctor Academy, Andover, New Hampshire, USA, July 29- Aug.3, 2001.
3. Marco Rincón, **Shi-You Ding**, Sheila McCrae, Jennifer Martin, Ed Bayer, Raphael Lamed, Yuval Shoham, Vincenzo Aurilia, and Harry Flint. Cellulosomal proteins assembly in rumen cellulolytic bacterium *Ruminococcus flavefaciens*. Proctor Academy, Andover, New Hampshire, USA, July 29- Aug.3, 2001.
4. **Ding, S.-Y.** cellulosomes in *Acetivibrio cellulolyticus* and *Bacteroides cellulosolvens*. Gordon Research Conference on Cellulases and Cellulosomes, Proctor Academy, Andover, New Hampshire, USA, July 25-30, 1999. (Oral presentation)

5. Ding, S-Y., Bayer, E. A., Shoham, Y. and Lamed, R., McCrae, S. I., Kirby, J., Aurilia, V., and Flint, H. J. Preliminary evidence of high-molecular-weight scaffoldin-like proteins from *Ruminococcus flavefaciens*. 3rd Carbohydrate Bioengineering Meeting, University of Newcastle Upon Tyne, UK, 11th-14th April 1999. P5.12
6. Ding, S-Y., Steiner, D., Kenig, R., Yaron, S., Morag, E., Shoham, Y., Bayer, E., Lamed, R. Evidence for cohesin and CBD domains, characteristic of cellulosomes in non-clostridial anaerobic bacteria. 8th International Symposium on the Genetics of Industrial Microorganisms, Jerusalem, Israel, June 28-July 2, 1998. p50.
7. Ding, S-Y., Steiner, D., Kenig, R., Yaron, S., Morag, E., Shoham, Y., Bayer, E., Lamed, R. Domain organization and sequence of the first non-clostridial scaffoldin from *Acetivibrio cellulolyticus*. Mie Bioforum, Genetics, biochemistry and ecology of cellulose degradation, Suzuka, Japan, Sept. 7-11, 1998. p47.
8. Ding, S-Y., Steiner, D Kenig, R Yaron, S., Morag, E Shoham, Y Bayer, E Lamed, R. Unique Cellulosome-related protein in *Bacteroides cellulosovens*. Mie Bioforum 98, Genetics, biochemistry and ecology of cellulose degradation, Suzuka, Japan, Sept. 7-11, 1998. p49.

CAZy - Carbohydrate-Active enZymes

Home Access by Family Access by Organism Acknowledgements Links Team CitingCAZy Search

Family GH5

Family GH5

CAZy Family Glycoside Hydrolase Family 5

Known Activities Endoglycosylceramidase (EC 3.2.1.123); β -mannosidase (EC 3.2.1.25); Cellulase (EC 3.2.1.4); Glucan 1,3- β -glucosidase (EC 3.2.1.58); Licheninase (EC 3.2.1.73); Glucan endo-1,6- β -glucosidase (EC 3.2.1.75); Mannan endo-1,4- β -mannosidase (EC 3.2.1.78); Endo-1,4- β -xylanase (EC 3.2.1.8); Cellulose 1,4- β -cellobiosidase (EC 3.2.1.91).

Mechanism Retaining

Catalytic Nucleophile/Base Glu (experimental)

Catalytic Proton Donor Glu (experimental)

3D Structure Status Available (see PDB). Fold (β/α)₈

Clan GH-A

Note formerly known as cellulase family A.

Relevant Links HOMSTRAD; InterPro; PFAM; PROSITE

Statistics CAZy(363); GenBank/GenPept (487); Swissprot (177); PDB (43); 3D(13); cryst(1)

Protein	Organism	EC#	GenBank / GenPept	SwissProt PDB / 3D
endo-1,4-glucanase	<i>Acidothermus cellulolyticus</i>	3.2.1.4	U33212 AAA75477.1 AX467594 CAD42489.1	P54583 1C0D A 1ECE A
endo-1,4-glucanase	<i>Actinomyces sp. 40</i>	3.2.1.4	U94825 AAC06196.1	O66064
xylanase	<i>Aeromonas caviae</i>	3.2.1.8	D88553 BAA13641.1	P70733
xylanase D	<i>Aeromonas caviae</i>	3.2.1.8	U86340 AAB63573.1	O24852
β -mannanase	<i>Agaricus bisporus</i>	3.2.1.78	Z50095 CAA90423.1	Q92401
exo-1,3-glucanase 1	<i>Agaricus bisporus</i>	3.2.1.58	X92961 CAA63536.1	Q12539
mannanase (Cel4A)	<i>Agaricus bisporus C54-carb8</i>	3.2.1.78	AJ271862 CAB76904.1	Q9P893
exo-1,3-glucanase 2 (fragment)	<i>Agaricus bisporus Horst U1</i>	3.2.1.58	X92961 CAA63537.1	Q12540
ORF PCZA361.14	<i>Amycolatopsis orientalis</i>	n.d.	AJ223998 CAA11771.1	O52801
endo-1,4-glucanase CelB	<i>Anaerocellum thermophilum</i>	3.2.1.4	Z86104 CAB06784.1	P96310
endo-1,4-glucanase CelD	<i>Anaerocellum thermophilum</i>	3.2.1.4	Z77855 CAB01405.1	Q59154
ORF At1g02310/T6A9.1	<i>Arabidopsis thaliana</i>	n.d.	AC064879 AAG00883.1 AY081352 AAL91241.1 BT002154 AAN72165.1 NC_003070 NP_171733.1	Q9FZ29

B

ORF At1g13130/F3F19.15	<i>Arabidopsis thaliana</i>	n.d.	AC007357 AAD31066.1 NM_101183 NP_172772.1		
ORF At2g20680	<i>Arabidopsis thaliana</i>	n.d.	AC006234 AAD20927.1	Q9SKU9	
ORF At3g10890/T7M13.3	<i>Arabidopsis thaliana</i>	n.d.	AC011708 AAF19560.1 NM_111926 NP_187700.1	Q9SG94	
ORF At3g10900/T7M13.2	<i>Arabidopsis thaliana</i>	n.d.	AC011708 AAF19559.1 NM_111927 NP_187701.1	Q9SG95	
ORF At3g26130/MTC11.2	<i>Arabidopsis thaliana</i>	n.d.	AB024038 BAB02432.1 NC_003074 NP_189244.1	Q9LTN0	
ORF At3g26140/MTC11.4	<i>Arabidopsis thaliana</i>	n.d.	AB024038 BAB02434.1 NC_003074 NP_189245.1	Q9LTM8	
ORF At3g30540/MQP15.4	<i>Arabidopsis thaliana</i>	n.d.	AB016878 BAB01021.1 NC_003074 NP_189675.1	Q9LW44	
ORF At4g28320	<i>Arabidopsis thaliana</i>	n.d.	AL161572 CAB79634.1 NM_118972 NP_194561.1	Q9M0H6	
ORF At5g01930/T20L15_200	<i>Arabidopsis thaliana</i>	n.d.	BT005831 AAO64766.1 AL162351 CAB82763.1 NM_120271 NP_195813.1	Q9LZV3	
ORF At5g16700/F5E19_40	<i>Arabidopsis thaliana</i>	n.d.	AL391147 CAC01834.1 NM_121675 NP_197172.1		
ORF At5g17500/K3M16_70	<i>Arabidopsis thaliana</i>	n.d.	AL391150 CAC01894.1 NM_121756 NP_197252.1		
ORF At5g66460/K1F13.12	<i>Arabidopsis thaliana</i>	n.d.	BT000452 AAN17429.1 AB013389 BAB10922.1 NM_126044 NP_201447.1	Q9FJZ3	
β -mannanase	<i>Aspergillus aculeatus</i>	3.2.1.78	L35487 AAA67426.1	Q00012	
endoglucanase II	<i>Aspergillus aculeatus</i>	n.d.	AF543446 AAN16396.1 AY173077 AAN75019.1		
FII-CMCase	<i>Aspergillus aculeatus</i>	3.2.1.4	AB015510 BAA29030.1	O74169	
endo-1,4-glucanase V	<i>Aspergillus aculeatus</i> WO 94/14953	3.2.1.4	AF054512 AAC08587.1	O59951	
endoglucanase A (EglA)	<i>Aspergillus kawachii</i>	n.d.	AB055431 BAB62317.1		
endoglucanase C (EglC)	<i>Aspergillus kawachii</i>	n.d.	AB055433 BAB62319.1		
endo-1,4-glucanase B (EglB)	<i>Aspergillus niger</i> CBS 120.49	3.2.1.4	AJ224452 AAE60102.1 AAE84292.1 CAA11965.1	O74706	
endoglucanase (Eng1)	<i>Aspergillus niger</i> IFO31125	3.2.1.4	AF331518 AAG50051.1		
unnamed protein product	<i>Aspergillus oryzae</i>	n.d.	AX011537 CAC07551.1		
ORF egl	<i>Azorhizobium caulinodans</i> ORS571	n.d.	Z48958 -		
endo-1,4-glucanase Cel5A	<i>Cel5A Bacillus agaradherans</i>	3.2.1.4	AF067428 AAC19169.1	O85465	1A3H _ 1E5J A 1H11 A 1H2J A 1H5V A 1HF5 A 1HF6 A 1HF7 A 1OCQ 1QHZ A 1QI0 A 1QI2 A 2A3H _ 3A3H _ 4A3H A 5A3H A 6A3H A 7A3H A 8A3H A
endoglucanase A (EngA)	<i>Bacillus amyloliquefaciens</i>	n.d.	AF363635 AAL99668.1		

UMAS1002					
β -mannanase	<i>Bacillus circulans</i> K-1	3.2.1.78	AB007123 BAA25878.1	O66185	
ORF BH0603	<i>Bacillus halodurans</i> C-125	n.d.	AP001509 BAB04322.1 NC_002570 NP_241469.1	Q9KF82	
endo-1,4-glucanase 3a	<i>Bacillus lautus</i>	3.2.1.4	A28175 CAA01935.1		
endo-1,4-glucanase B	<i>Bacillus lautus</i>	3.2.1.4	M33762 AAA22408.1 A28172 CAA01934.1	P23550	
endo-1,4-glucanase	<i>Bacillus polymyxa</i>	3.2.1.4	M33791 AAA22631.1	P23548	
unnamed protein product	<i>Bacillus</i> sp.	n.d.	- AAE86309.1 AX665431 CAD82874.1		
unnamed protein product	<i>Bacillus</i> sp.	n.d.	AX643592 CAD67813.1		
endo-1,4-glucanase	<i>Bacillus</i> sp. 1139	3.2.1.4	M15743 AAA22305.1 D00066 BAA00045.1	P06564	
endo-1,4-glucanase	<i>Bacillus</i> sp. 22-28	3.2.1.4	D85236 BAA12744.1	Q45554	
endo-1,4-glucanase	<i>Bacillus</i> sp. 5H	3.2.1.4	AB016164 BAA31712.1	O83012	
CelS	<i>Bacillus</i> sp. 79-23	3.2.1.4	AF045482 AAC02536.1	O52731	
endo-1,4-glucanase A	<i>Bacillus</i> sp. BP-23	3.2.1.4	Y12512 CAA73113.1	O08342	
cellulase	<i>Bacillus</i> sp. CBS 670.93	3.2.1.4	A76937 CAB58698.1 A79880 CAB59165.1 AX665429 CAD82873.1		1LF1 A
endo-1,4-glucanase	<i>Bacillus</i> sp. D04	3.2.1.4	U27084 AAC43478.1	Q45430	
endo-1,4-glucanase	<i>Bacillus</i> sp. KSM-635	3.2.1.4	M27420 AAA22304.1	P19424	1G01 A 1G0C A
endo-1,4-glucanase	<i>Bacillus</i> sp. KSM-64	3.2.1.4	M84963 AAA73189.1	Q59241	
endoglucanase N252 (Egl252)	<i>Bacillus</i> sp. KSM-N252	3.2.1.4	AB057671 BAB62295.1		
cellulase	<i>Bacillus</i> sp. KSM-S237	3.2.1.4	AB018420 BAB19360.1		
endo-1,4-glucanase A	<i>Bacillus</i> sp. N-4	3.2.1.4	M14781 AAA22301.1	P06566	
endo-1,4-glucanase B	<i>Bacillus</i> sp. N-4	3.2.1.4	M14729 AAA22299.1	P06565	
endo-1,4-glucanase C	<i>Bacillus</i> sp. N-4	3.2.1.4	M25500 AAA22306.1	P19570	
endo-1,4-glucanase B1	<i>Bacillus</i> sp. N186-1	3.2.1.4	Z33876 CAA83942.1	Q59232	
cellulase (CelA)	<i>Bacillus</i> sp. NBL420	n.d.	AY039744 AAK73277.1		
endo-1,4-glucanase	<i>Bacillus subtilis</i>	3.2.1.4	M28332 AAA22307.1	Q45532	
endo-1,4-glucanase	<i>Bacillus subtilis</i> BSE616	3.2.1.4	D01057 BAA00859.1	P23549	
endo-1,4- β -glucanase	<i>Bacillus subtilis</i> CHZ1	3.2.1.4	AY044252 AAK94871.1		
endo-1,4-glucanase	<i>Bacillus subtilis</i> DLG	3.2.1.4	M16185 AAA22496.1	P07983	
endo-1,4-glucanase (EglS or BglC)	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	3.2.1.4	AF355629 AAK39540.1 X04689 CAA28392.1 X67044 CAA47429.1 Z29076 CAA82317.1 Z73234 CAA97610.1 Z99113 CAB13696.1 NC_000964 NP_389695.1	P10475	
ORF YnfF	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	n.d.	Z73234 CAA97612.1 Z99113 CAB13698.1	Q45070	
endo-1,4-glucanase	<i>Bacteroides rumenicola</i>	3.2.1.4	M38216 AAA22909.1	Q44878	
BT3043	<i>Bacteroides thetaiotaomicron</i> VPI-5482	n.d.	AE016938 AAO78149.1 NC_004663 NP_811955.1		
BL0157	<i>Bifidobacterium longum</i> NCC2705	n.d.	AE014632 AAN24012.1 NC_004307 NP_695376.1		
BL1333	<i>Bifidobacterium longum</i> NCC2705	n.d.	AE014762 AAN25133.1 NC_004307 NP_696497.1		
BL1761	<i>Bifidobacterium longum</i> NCC2705	n.d.	AE014810 AAN25544.1 NC_004307 NP_696908.1		
β -1,3-glucanase	<i>Blumeria graminis</i>	3.2.1.-	AF317734 AAL26905.1		
blr3367	<i>Bradyrhizobium japonicum</i> USDA110	n.d.	AP005947 BAC48632.1 NC_004463 NP_770007.1		

3

endo-1,4-glucanase A		<i>Butyrivibrio fibrisolvens</i> A46	3.2.1.4	M37031 AAA20893.1	P22541	
endo-1,4-glucanase 1		<i>Butyrivibrio fibrisolvens</i> H17c	3.2.1.4	X17538 CAA35574.1	P20847	
β -1,4-mannanase (ManA)		<i>Caldibacillus cellulovorans</i>	3.2.1.78	AF163837 AAF22274.1	Q9RFX5	
β -mannanase/endo-1,4-glucanase		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.4 3.2.1.78	L01257 AAA71887.1 M36063 AAA72861.1	P22533	
endo-1,4-glucanase/cellobiohydrolase		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.91 3.2.1.4	X13602 CAA31936.1	P10474	
CelB (multidomain protein)		<i>Caldicellulosiruptor sp. Tok7B.1</i>	n.d.	AF078737 AAD30364.1	Q9X3P6	
exo-1,3-glucanase		<i>Candida albicans</i>	3.2.1.58	X56556 CAA39908.1	P29717	1CZ1 A 1EQC A 1EQP A
1,3- β -glucanase (EXG1) ORF CC0801		<i>Candida oleophila</i> <i>Caulobacter crescentus</i> CB15	n.d. n.d.	AF393806 AAM21469.1 AE005756 AAK22786.1 NC_002696 NP_419618.1	Q9AA10	
endo-1,4-glucanase D	Cel5A	<i>Cellulomonas fimi</i>	3.2.1.4	L02544 AAA23089.1	P50400	
endo-1,4-glucanase B (cflB)		<i>Cellulomonas flavigena</i>	3.2.1.4	AF172345 AAD48494.2		
endo-b1,4-mannanase 5A	Man5A	<i>Cellvibrio japonicus</i>	n.d.	AY187031 AAO31759.1		
endo-b1,4-mannanase 5B	Man5B	<i>Cellvibrio japonicus</i>	n.d.	AY187032 AAO31760.1		
endo-b1,4-mannanase 5C	Man5C	<i>Cellvibrio japonicus</i>	n.d.	AY187033 AAO31761.1		
cellodextrinase C		<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)	3.2.1.-	X61299 CAA43597.1	P27033	
endo-1,4-glucanase E		<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)	3.2.1.4	X86798 CAA60493.1	Q59665	
endo-1,4-glucanase A		<i>Cellvibrio mixtus</i>	3.2.1.4	AF003696 AAB61461.1	O07652	
endo-1,4-glucanase B		<i>Cellvibrio mixtus</i>	3.2.1.4	AF003697 AAB61462.2	O07653	
ORF manB (fragment)		<i>Chlorella vulgaris</i> C-169	n.d.	AB036816 BAA99563.1		
Cellulase CelA		<i>Clavibacter michiganensis</i> NCPPB 382	3.2.1.4	X62582 CAA44467.2	Q9K5C7	
cellulase CelA		<i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i>	3.2.1.4	AY007311 AAK16222.1	Q9AF65	
endo-1,4-glucanase C307		<i>Clostridium sp. F1</i>	3.2.1.4	D00945 BAA00793.1	P23340	
endo-1,4-glucanase		<i>Clostridium acetobutylicum</i>	3.2.1.4	M31311 AAA23230.1	P15704	
ORF CAC0706		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007585 AAK78683.1	Q97L56	
ORF CAC0825		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007598 AAK78801.1	Q97KU1	
ORF CAC0826		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007598 AAK78802.1	Q97KU0	
ORF CAC0912		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007607 AAK78888.1	Q97KK6	
ORF CAC0918		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007607 AAK78894.1	Q97KK1	
ORF CAC3469		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE007844 AAK81397.1	Q97DK6	
ORF CAP0118		<i>Clostridium</i>	n.d.	AE001438 AAK76863.1	Q97TI3	

		<i>ac. tobutylicum</i> ATCC 824		NC_001988 NP_149281.1	
ORF CAP0119		<i>Clostridium acetobutylicum</i> ATCC 824	n.d.	AE001438 AAK76864.1 NC_001988 NP_149282.1	Q97TI2
β -1,4-glucanase (Cel5I)	Cel5I	<i>Clostridium cellulolyticum</i>	n.d.	AY077754 AAL79562.1	
cellulase CelIN		<i>Clostridium cellulolyticum</i>	3.2.1.4	AF316823 AAG45162.1	Q9EYQ0
endo-1,4-glucanase A		<i>Clostridium cellulolyticum</i>	3.2.1.4	M32362 AAA23221.1 M93096 AAA51444.1	P17901 1EDG _
endo-1,4-glucanase D		<i>Clostridium cellulolyticum</i>	3.2.1.4	D90341 BAA14354.1	P25472
mannanase ManK		<i>Clostridium cellulolyticum</i>	3.2.1.78	AF316823 AAG45159.1	Q9EYQ3
endo-1,4-glucanase 5A (EngF)	Cel5A	<i>Clostridium cellulovorans</i>	3.2.1.4	U37056 AAB40891.1	P94622 3D
endo-1,4-glucanase B		<i>Clostridium cellulovorans</i>	3.2.1.4 3.2.1.8 3.2.1.73	M75706 AAA23231.1	P28621
endo-1,4-glucanase D		<i>Clostridium cellulovorans</i>	3.2.1.4	M37434 AAA23233.1	P28623
endo-1,4-glucanase E (EngE)		<i>Clostridium cellulovorans</i>	3.2.1.4	AF105331 AAD39739.1	Q9XD99
mannanase A (ManA)		<i>Clostridium cellulovorans</i>	3.2.1.78	AF132735 AAF06110.2	
endo-1,4-glucanase A		<i>Clostridium josui</i>	3.2.1.4	D85526 BAA12826.1	Q59290
endo-1,4-glucanase (CelA)		<i>Clostridium longisporum</i>	3.2.1.4	L02868 AAC37035.1	P54937
endo-1,4-glucanase E	Cel5C	<i>Clostridium thermocellum</i>	3.2.1.4	M22759 AAA23224.1	P10477
1,4- β -cellobiohydrolase (CelO)		<i>Clostridium thermocellum F7</i>	3.2.1.91	AJ275975 CAB76938.1	
endo-1,4-glucanase C (CelC)		<i>Clostridium thermocellum F7</i>	3.2.1.4	AJ307315 CAC27410.1	
endo-1,4-glucanase B	Cel5A	<i>Clostridium thermocellum</i> NCIB 10682	3.2.1.4	X03592 CAA27266.1	P04956
endo-1,4-glucanase C	Cel5B	<i>Clostridium thermocellum</i> NCIB 10682	3.2.1.4	M19422 AAA23220.1	P07985 1CEC _ 1CEN _ 1CEO _
endo-1,4-glucanase G	Cel5D	<i>Clostridium thermocellum</i> NCIB 10682	3.2.1.4	X69390 CAA49187.1	Q05332
endo-1,4-glucanase H (CelH)	Cel26A-Cel5E	<i>Clostridium thermocellum</i> NCIB 10682	3.2.1.4	M31903 AAA23225.1	P16218
exo-1,3- β -glucanase		<i>Cochliobolus carbonum</i>	3.2.1.58	AF229446 AAF65310.1	
endo-1,4-glucanase 1		<i>Cryptococcus flavus</i>	3.2.1.4	S45137 AAC60541.1 D13967 BAA03070.1	Q04469
exo- β -1,3-glucanase (fragment)		<i>Cryptococcus neoformans</i> var. <i>neoformans</i>	n.d.	AF243533 AAM26269.1	
endo- β -mannanase (fragment)		<i>Datura ferox</i>	n.d.	AF323949 AAO06964.1	
exo-1,3-glucanase		<i>Debaryomyces occidentalis</i> (<i>S. occidentalis</i>)	3.2.1.58	Z46871 CAA86951.1	Q12700
endo-1,4-glucanase A (eglA)		<i>Emericella nidulans</i>	3.2.1.4	AB009402 BAA82592.1	
cellulase CelA		<i>Epidinium caudatum</i>	n.d.	AB104618 BAC57895.1	

endo-1,4-glucanase	<i>Epidinium caudatum</i>	3.2.1.4	AB011273 BAA76394.1	
endoglucanase Epi2	<i>Epidinium caudatum</i>	n.d.	AB104616 BAC57893.1	
endo-1,4-glucanase N	<i>Erwinia carotovora atroseptica</i>	3.2.1.4	L39788 AAC37033.1	Q59394
endo-1,4-glucanase V1	<i>Erwinia carotovora</i> SCC3193	3.2.1.4	X79241 CAA55823.1	Q59395
endo-1,4-glucanase V	<i>Erwinia carotovora</i> SCRI193	3.2.1.4	X76000 CAA53592.1	Q47096
endo-1,4-glucanase CelA (fragment)	<i>Erwinia carotovora subsp. carotovora</i> LY34	3.2.1.4	AF025768 AAC02964.1	O31029
xylanase	<i>Erwinia chrysanthemi</i>	3.2.1.8	U41750 AAB53151.1	Q46961 1NOF
endo-1,4-glucanase Z	<i>Cel5A Erwinia chrysanthemi</i> 3937	3.2.1.4	Y00540 CAA68604.1	P07103 1EGZ A
endo-1,4-glucanase 3	<i>Fibrobacter intestinalis</i>	3.2.1.4	L39840 AAA92982.1	Q59440
endo-1,4-glucanase 3	<i>Fibrobacter succinogenes</i>	3.2.1.4	M29047 AAA24893.1	P14250
endo-1,4-glucanase G	<i>Fibrobacter succinogenes</i>	3.2.1.4	U33887 AAB38548.1	Q47916
cellodextrinase A (CedA)	<i>Fibrobacter succinogenes</i> S85	3.2.1.-	U07419 AAA50210.1	Q59441
CMC-xylanase (fragment)	<i>Fibrobacter succinogenes</i> S85	3.2.1.4	U94826 AAC06197.1	O66065
cellulase (Celc)	<i>Filobasidiella neoformans</i> 309 Cap67	n.d.	AJ486863 CAD31110.1	
β -mannanase	<i>Geobacillus stearothermophilus</i> MCA2184	3.2.1.78	AF038547 AAC71692.1	
endoglucanase 1 (Eng1)	<i>Globodera rostochiensis</i>	3.2.1.4	AF004523 AAC48325.1 AF056110 AAC63988.1	O16028
endoglucanase 2 (Eng2)	<i>Globodera rostochiensis</i>	3.2.1.4	AF004716 AAC48341.1 AF056111 AAC63989.1	O44078
β -1,4-endoglucanase precursor (Eng-3)	<i>Globodera rostochiensis</i> Ro-1 Mierenbos	3.2.1.4	AF408154 AAN03645.1 AF408155 AAN03646.1	
β -1,4-endoglucanase precursor (Eng-4)	<i>Globodera rostochiensis</i> Ro-1 Mierenbos	3.2.1.4	AF408156 AAN03647.1 AF408157 AAN03648.1	
endoglucanase 1 (Eng1)	<i>Heterodera glycines</i>	3.2.1.4	AF052733 AAC15707.1 AF006052 AAC48327.1 A79341 CAB59144.1	O18453
endoglucanase 2 (Eng2)	<i>Heterodera glycines</i>	3.2.1.4	AF006053 AAC48326.1 A79340 CAB59143.1	O18454
endoglucanase 3	<i>Heterodera glycines</i>	3.2.1.4	AF044210 AAC33848.1 AF056048 AAC33860.1	O77449
ndoglucanase 4	<i>Heterodera glycines</i>	3.2.1.4	AY043224 AAK85303.1	
endo-1,4-glucanase	<i>Humicola grisea</i>	3.2.1.4	D84470 BAA12676.1	Q12620
endo-1,4-glucanase IV	<i>Humicola insolens</i>	3.2.1.4	X76046 CAA53631.1	Q12624
β -1,6-glucanase precursor (Bgn3)	<i>Hypocrea virens</i>	n.d.	AF395757 AAL84696.1	
exo-1,3-glucanase	<i>Kluyveromyces lactis</i>	3.2.1.58	Z46869 CAA86949.1	Q12628
mannanase (Lm1)	<i>Lactuca sativa</i>	n.d.	AJ315978 CAC51690.1 AJ315978 CAC51690.2	Q93X40
Xyl38	<i>Leptosphaeria maculans</i>	n.d.	AF487263 AAO49459.1	
LB251	<i>Leptospira interrogans</i> serovar lai str. 56601	n.d.	AE011612 AAN51810.1 NC_004343 NP_714795.1	
β -1,4-mannanase (Man2)	<i>Lycopersicon esculentum</i>	3.2.1.78	AF184238 AAG00315.1	
β -mannanase	<i>Lycopersicon esculentum</i>	3.2.1.78	AF017144 AAB87859.1	O48540
endo- β -mannanase	<i>Lycopersicon esculentum</i>	3.2.1.78	AY034075 AAK56557.1 AY046589 AAK97759.2	

endo-1,4-glucanase 1	<i>Macrophomina phaseolina</i>	3.2.1.4	AY046588 AAK97760.1 U14948 AAB51451.1	Q12638	
endo-1,4-glucanase 2	<i>Macrophomina phaseolina</i>	3.2.1.4	U13914 AAB03889.1	Q12637	
β -1,4-endoglucanase Eng-1i (fragment)	<i>Meloidogyne arenaria</i>	3.2.1.4	AF323097 AAK21892.1		
β -1,4-endoglucanase Eng-1ii (fragment)	<i>Meloidogyne arenaria</i>	3.2.1.4	AF323098 AAK21893.1		
β -1,4-endoglucanase Eng-1i (fragment)	<i>Meloidogyne hapla</i>	3.2.1.4	AF323096 AAK21891.1		
β -1,4-endoglucanase Eng-1a	<i>Meloidogyne incognita</i>	3.2.1.4	AF323087 AAK21882.1	Q9BJZ1	
β -1,4-endoglucanase Eng-1i (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323090.1 AAK21885.1		
β -1,4-endoglucanase Eng-1ii (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323091 AAK21886.1		
β -1,4-endoglucanase Eng-1iii (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323092 AAK21887.1		
β -1,4-endoglucanase Eng-1iv (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323093 AAK21888.1		
β -1,4-endoglucanase Eng-1v (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323094 AAK21889.1		
β -1,4-endoglucanase Eng-1vi (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323095 AAK21890.1		
β -1,4-endoglucanase Eng-2 (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323086 AAK21881.1		
β -1,4-endoglucanase Eng-2a	<i>Meloidogyne incognita</i>	3.2.1.4	AF323088 AAK21883.2		
β -1,4-endoglucanase Eng-2b (fragment)	<i>Meloidogyne incognita</i>	3.2.1.4	AF323089.1 AAK21884.1		
endo-1,4-glucanase 1 (Eng-1)	<i>Meloidogyne incognita</i>	3.2.1.4	AF100549 AAD45868.1	Q9UA57	
xylanase (Xyl-1)	<i>Meloidogyne incognita</i>	3.2.1.8	AF224342 AAF37276.1		
β -1,4-endoglucanase Eng-1i (fragment)	<i>Meloidogyne javanica</i>	3.2.1.4	AF323099 AAK21894.1		
β -1,4-endoglucanase Eng-1ii (fragment)	<i>Meloidogyne javanica</i>	3.2.1.4	AF323100 AAK21895.1		
Mr2086	<i>Mesorhizobium loti</i> MAFF303099	n.d.	NC_002678 NP_103519.1		
Mr3893	<i>Mesorhizobium loti</i> MAFF303099	n.d.	NC_002678 NP_104903.1		
endo-1,4-mannanase	<i>Mytilus edulis</i>	3.2.1.78	AJ271365 CAC81056.1		cryst
endo-1,4-glucanase A	<i>Neocallimastix frontalis</i>	3.2.1.4	U38843 AAC63094.1	Q01409	
endo-1,4-glucanase B (CelB)	<i>Neocallimastix patriciarum</i>	3.2.1.4	X77186 AAE59927.1 Z31364 CAA83238.1 CAA83238.1	Q12647	
endo-1,4-glucanase D (CelD)	<i>Neocallimastix patriciarum</i>	3.2.1.4	AF053363 AAC06321.1	O59943	
β -1,6-glucanase	<i>Neotyphodium</i> sp. FFCB_2002	3.2.1.75	AF535131 AAN04103.1		
ORF B23L21.220	<i>Neurospora crassa</i>	n.d.	AL356172 CAB91690.1		
ORF Alr0290	<i>Nostoc</i> sp. PCC 7120	n.d.	AP003581 BAB77814.1 NC_003272 NP_484334.1		
endo-1,4-glucanase	<i>Orpinomyces joyonii</i>	3.2.1.4	U59432 AAC49731.1	P87211	
endo-1,4-glucanase CelB	<i>Orpinomyces joyonii</i>	3.2.1.4	AF015249 AAB69348.1	O13334	
endo-1,4-glucanase CelB29	<i>Orpinomyces joyonii</i>	3.2.1.4	AF015248 AAB69347.1	O13333	

endo-1,4-glucanase B	<i>Orpinomyces</i> sp. PC-2	3.2.1.4	U57818 AAD04193.1 AAE59925.1	P78719
mannanase ManA	<i>Orpinomyces</i> sp. PC-2	n.d.	AF177206 AAL01213.1	
OJ1208D02.11	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	n.d.	AC107314 AAM08620.1	
OJ1208D02.5 or OJ1003C07.1	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	n.d.	AC107314 AAM08614.1 AC113335 AAM08821.1	
OSJNBa0010E04.2	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	n.d.	AC096687 AAL79758.1	
OSJNBa0010E04.20	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	n.d.	AC096687 AAL79761.1	
OSJNBb0011N17.6	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	n.d.	AL606614 CAD41089.1	
OSJNBb0011N17.7	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	n.d.	AL606614 CAD41090.1	
OSJNBb0011N17.8	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	n.d.	AL606614 CAD41091.1	
P0481E12.1	<i>Oryza sativa</i>	n.d.	AP003076 BAB56016.1	
(OSJNBa0014K08.29)	(<i>japonica</i> cultivar-group)	n.d.	AP003376 BAC05600.1	
P0671D01.24	<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)	n.d.	AP003284 BAB91747.1	
endo- β -1,4-glucanase	<i>Paenibacillus</i> sp. KCTC8848P	n.d.	AF345984 AAL83749.1	
43 kDa glycoprotein	<i>Paracoccidioides</i> <i>brasiliensis</i> B339	n.d.	U26160 AAC49253.1	Q01575
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41620 (=Pb-9)	n.d.	AB047690 BAB12190.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41621 (=Pb-18)	n.d.	AB047691 BAB12191.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41624 (=Bt-4)	n.d.	AB047693 BAB12193.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41626 (=Bt-9)	n.d.	AB047694 BAB12194.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM41632	n.d.	AB047695 BAB12195.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46215	n.d.	AB047696 BAB12196.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46463 (=Tatu)	n.d.	AB047700 BAB12200.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46465 (=Pb-267)	n.d.	AB047692 BAB12192.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46467	n.d.	AB047699 BAB12199.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46468(P-25)	n.d.	AB047698 BAB12198.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM46930	n.d.	AB047697 BAB12197.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM47183 (=PRT1-Tatu 1)	n.d.	AB047701 BAB12201.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides</i> <i>brasiliensis</i> IFM47185 (=PRT2 Y)	n.d.	AB047702 BAB12202.1	
43 kDa glycoprotein (Gp43)	<i>Paracoccidioides</i>	n.d.	AB047704 BAB12204.1	

(fragment)	<i>brasiliensis IFM47217</i> (=D4S1=Tatu 4)			
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides brasiliensis IFM47217</i> (=D4S9)	n.d.	AB047703 BAB12203.1	
43 kDa glycoprotein (Gp43) (fragment)	<i>Paracoccidioides brasiliensis IFM47247</i> (=D4LIV1)	n.d.	AB047705 BAB12205.1	
endo-xylanase (XynA)	<i>Pectobacterium chrysanthemi P860219</i>	n.d.	AY055730 AAL16415.1	
endo-1,4-glucanase II	<i>Penicillium janthinellum</i>	3.2.1.4	X89564 CAA61740.1	Q12665
ORF Exo1	<i>Phytophthora infestans</i>	n.d.	AF494014 AAM18483.1	
ORF Exo2	<i>Phytophthora infestans</i>	n.d.	AF494016 AAM18485.1	
ORF Exo3	<i>Phytophthora infestans</i>	n.d.	AF494015 AAM18484.1	
exo-1,3-glucanase	<i>Pichia angusta</i>	3.2.1.58	Z46868 CAA86948.1	Q12626
exo-1,3-glucanase	<i>Pichia anomala K</i>	3.2.1.58	AJ222862 CAA11018.1	O83983
endoglucanase 5A	<i>Cel5A Piromyces equi</i>	3.2.1.4	AJ277483 CAB92326.1	
endoglucanase (egl-1)	<i>Piromyces rhizinflata</i>	3.2.1.4	AF165266 AAD43818.1	Q9Y870
cellulase CelA (fragment)	<i>Polyplastron multivesiculatum</i>	n.d.	AB104619 BAC57896.1	
endo-1,4-glucanase	<i>Prevotella ruminicola</i>	3.2.1.4	AB022867 BAA74515.1	Q9ZN63
endo-1,4-glucanase (ORF4)	<i>Prevotella ruminicola</i>	3.2.1.4	U96771 AAC97596.1	O06842
xylanase	<i>Prevotella ruminicola</i>	3.2.1.8	M83379 AAC36862.1	Q45397
cellulase (PhEG)	<i>Psacothoea hilaris</i>	n.d.	AB080266 BAB86867.1	
CelG	<i>Pseudoalteromonas haloplanktis A23</i>	3.2.1.4	Y17552 CAA76775.1	O86099
PP1682	<i>Pseudomonas putida KT2440</i>	n.d.	AE016780 AAN67303.1 NC_002947 NP_743839.1	
β -1,4-mannanase (AmnA)	<i>Pseudomonas sp. ND137</i>	n.d.	AB063258 BAB79290.1 AB063258 BAB79290.2	
cellulase (AclA)	<i>Pseudomonas sp. ND137</i>	n.d.	AB063256 BAB79288.1	
PSPTO0905	<i>Pseudomonas syringae pv. tomato str. DC3000</i>	n.d.	AE016859 AAO54439.1 NC_004578 NP_790744.1	
PSPTO3292	<i>Pseudomonas syringae pv. tomato str. DC3000</i>	n.d.	AE016867 AAO56770.1 NC_004578 NP_793075.1	
ORF PAB0632	<i>Pyrococcus abyssi</i>	n.d.	AJ248285 CAB49854.1 NC_000868 NP_126623.1	Q9V052
endoglucanase (PH1171)	<i>Pyrococcus horikoshii OT3</i>	3.2.1.4	AP000005 BAA30271.1 NC_000961 NP_143072.1	O58925
endo-1,4-glucanase	<i>Ralstonia solanacearum AW</i>	3.2.1.4	M84922 AAA61980.1	P17974
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP2047</i>	n.d.	AF295262 AAK97112.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP2957</i>	n.d.	AF295265 AAK97115.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP2958</i>	n.d.	AF295266 AAK97116.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP2972</i>	n.d.	AF295264 AAK97114.1	
endoglucanase	<i>Ralstonia solanacearum CFBP3059</i>	n.d.	AF295270 AAK97120.1	
endoglucanase (fragment)	<i>Ralstonia solanacearum CFBP3858</i>	n.d.	AF295259 AAK97109.1	
ndoglucanase (fragment)	<i>Ralstonia solanacearum CFBP712</i>	n.d.	AF295267 AAK97117.1	
ndoglucanase (fragment)	<i>Ralstonia solanacearum CFBP715</i>	n.d.	AF295268 AAK97118.1	
endoglucanase	<i>Ralstonia solanacearum</i>	n.d.	AF295274 AAK97124.1	

	CFBP734				
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> GMI1000	n.d.	AF295251 AAK97101.1		
ORF Egl	<i>Ralstonia solanacearum</i> GMI1000	3.2.1.4	AL646076 CAD17313.1 NC_003296 NP_521723.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> ICMP7963	n.d.	AF295263 AAK97113.1		
endoglucanase	<i>Ralstonia solanacearum</i> J25	n.d.	AF295279 AAK97129.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> J25	n.d.	AF295276 AAK97126.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> JT516	n.d.	AF295258 AAK97108.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> JT523	n.d.	AF295252 AAK97102.1		
endoglucanase	<i>Ralstonia solanacearum</i> JT525	n.d.	AF295272 AAK97122.1		
endoglucanase	<i>Ralstonia solanacearum</i> JT528	n.d.	AF295273 AAK97123.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> MAFF211266	n.d.	AF295250 AAK97100.1		
endoglucanase	<i>Ralstonia solanacearum</i> NCPB1018	n.d.	AF295271 AAK97121.1		
endoglucanase	<i>Ralstonia solanacearum</i> NCPB283	n.d.	AF295275 AAK97125.1		
ndoglucanase (fragment)	<i>Ralstonia solanacearum</i> NCPB3190	n.d.	AF295253 AAK97103.1		
endoglucanase	<i>Ralstonia solanacearum</i> NCPB342	n.d.	AF295278 AAK97128.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> NCPB3987	n.d.	AF295261 AAK97111.1		
endoglucanase	<i>Ralstonia solanacearum</i> NCPB505	n.d.	AF295277 AAK97127.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> R230	n.d.	AF295280 AAK97130.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> R292	n.d.	AF295255 AAK97105.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW151	n.d.	AF295254 AAK97104.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW162	n.d.	AF295256 AAK97106.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW469	n.d.	AF295269 AAK97119.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW477	n.d.	AF295260 AAK97110.1		
endoglucanase (fragment)	<i>Ralstonia solanacearum</i> UW9	n.d.	AF295257 AAK97107.1		
endoglycoceramidase	<i>Rhodococcus</i> sp. C9	3.2.1.123	AB042327 BAB17317.1		
endoglycoceramidase II	<i>Rhodococcus</i> sp. M-777	3.2.1.123	U39554 AAB67050.1	O33853	
endo-1,4-glucanase I	<i>Robillarda</i> sp. Y-20 (<i>Pestalotiopsis</i> sp.)	3.2.1.4	AB030819 BAA90480.1	P23044	
ndo-1,4-glucanase 4	<i>Ruminococcus albus</i>	3.2.1.4	AB016777 BAA32286.1 D16315 BAA32286.1	Q07940	
endo-1,4-glucanase A	<i>Ruminococcus albus</i>	3.2.1.4	L10243 AAA26467.1 X54931 CAA38692.1	P23660 Q59733	
endo-1,4-glucanase B	<i>Ruminococcus albus</i>	3.2.1.4	X54932 CAA38693.1	P23661	
endo-1,4-glucanase I	<i>Ruminococcus albus</i>	3.2.1.4	M30928 AAA26469.1	P16216	
xylanase (fragment)	<i>Ruminococcus albus</i>	n.d.	AB057589 BAB39494.1 AB057589 BAB39495.1		
β -1,4-endoglucanase VII	<i>Ruminococcus albus</i> F-	3.2.1.4	AB028321 BAA92430.1		

(EgVII)	40			
endo-1,4-glucanase V (EgV)	<i>Ruminococcus albus</i> F-40	3.2.1.4	AB028320 BAA92146.1	
endo-1,4-glucanase A (EndA)	<i>Ruminococcus flavefaciens</i> 17	3.2.1.4	S55178 AAB19708.1 Z83304 CAB05881.1	O05143 Q53302
cellodextrinase	<i>Ruminococcus flavefaciens</i> FD-1	3.2.1.-	X51944 CAA36207.1	P16169
EXG1	<i>Saccharomyces bayanus</i> 623-6C	n.d.	AY144818 AAO32382.1	
SPR1	<i>Saccharomyces bayanus</i> 623-6C	n.d.	AY144819 AAO32383.1	
EXG1 (fragment)	<i>Saccharomyces castellii</i> CBS4309	n.d.	AY144925 AAO32489.1	
EXG1 (fragment)	<i>Saccharomyces castellii</i> CBS4309	n.d.	AY144926 AAO32490.1	
exo-1,3-glucanase (sporulation)	<i>Saccharomyces cerevisiae</i> GRF88	3.2.1.58	S52935 AAB24895.1 X59259 CAA41952.1 Z75098 CAA99399.1	P32603
exo-1,3-glucanase 1	<i>Saccharomyces cerevisiae</i> S288C	3.2.1.58	M34341 AAA34599.1 U17243 AAB67345.1 NC_001144 NP_013403.1	P23776
exo-1,3-glucanase 2	<i>Saccharomyces cerevisiae</i> S288C	3.2.1.58	Z46870 CAA86950.1 Z68329 CAA92719.1 Z70202 CAA94100.1 NC_001136 NP_010547.1	P52911
ORF YBR056W	<i>Saccharomyces cerevisiae</i> S288C	n.d.	Z35925 CAA84999.1 Z46260 CAA86399.1 NC_001134 NP_009612.1	P38081
ORF YIB7W	<i>Saccharomyces cerevisiae</i> S288C	n.d.	Z37996 CAA86077.1 Z38062 CAA86209.1 NC_001141 NP_012272.1	P40566
EXG1	<i>Saccharomyces kluyveri</i> CBS3082	n.d.	AY145000 AAO32563.1	
endo-1,4-glucanase I (fragment)	<i>Schizophyllum commune</i>	3.2.1.4		P81190
exo-1,3-glucanase (SPAC12B10.11)	<i>Schizosaccharomyces pombe</i> 972h-	3.2.1.58	Z70721 CAA94701.1 NC_003424 NP_594643.1	Q10444
ORF SPBC1105.05	<i>Schizosaccharomyces pombe</i> 972h-	n.d.	AL096851 CAB50968.1 NC_003423 NP_596461.1	
ORF SPBC2D10.05	<i>Schizosaccharomyces pombe</i> 972h-	n.d.	NC_003423.1 NP_596224.1	
endoglucanase S (EndS)	<i>Sinorhizobium meliloti</i>	3.2.1.4	AF233448 AAG44364.1	
cellulase	<i>Stigmatella aurantiaca</i> Sg a15	n.d.	AJ421825 CAD19084.1	
ORF ManA2 (SC2H4.16)	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL031514 CAA20610.1 NC_003888 NP_630335.1	O86599
ORF SC10F4.10c	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL450350 CAC16970.1 NC_003888 NP_631677.1	Q9F3Q0
ORF SC6D11.02c	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL158061 CAB76325.1 NC_003888 NP_631455.1	
ORF SCF11.34c (ManA)	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL121746 CAB57406.1 AL132662 CAB59611.1 AL939106 CAD55266.1	
ORF SCF51A.35	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL121596 CAB56687.1 NC_003888 NP_624777.1	
ORF SCM11.04c	<i>Streptomyces coelicolor</i> A3(2)	n.d.	AL133278 CAB61915.1 NC_003888 NP_625246.1	
chitosanase II (Choll)	<i>Streptomyces griseus</i> HUT 6037	3.2.1.132	AB088201 BAC65342.1	
endo-1,4-glucanase	<i>Streptomyces lividans</i>	3.2.1.4	M82807 -	P27035
β -mannanase	<i>Streptomyces lividans</i>	3.2.1.78	M92297 AAA26710.1	P51529

ORF SSO3007	66	<i>Sulfolobus solfataricus</i>	n.d.	AE006891 AAK43109.1 AL512980 CAC24030.1 NC_002754 NP_344319.1		
endo- β -1,4 glucanase (Eg1)		<i>Talaromyces emersonii</i>	3.2.1.4	AF440003 AAL33630.1 AF440013 AAL33639.1		
ORF TTE0061		<i>Thermoanaerobacter tengcongensis MB4T</i>	n.d.	AE012980 AAM23368.1	Q8RDH1	
ORF TTE0359		<i>Thermoanaerobacter tengcongensis MB4T</i>	n.d.	AE013009 AAM23649.1	Q8RCQ7	
β -mannanase A		<i>Thermoanaerobacterium polysaccharolyticum KM-THCJ</i>	3.2.1.78	U82255 AAD09354.1	Q9ZA17	
β -1,4-glucanase (ENG1)		<i>Thermoascus aurantiacus IFO 9748</i>	3.2.1.4	AY055121 AAL16412.1 AF487830 AAL88714.2		1GZJ A 1H1N A
endo-1,4-glucanase E5	Cel5A	<i>Thermobifida fusca</i>	3.2.1.4	L01577 AAC09379.1	Q01786	
β -mannanase (Man)		<i>Thermobifida fusca (Thermomonospora fusca)</i>	3.2.1.78	AJ006227 CAA06924.1		1BQC A 2MAN A 3MAN A
endo-1,4-glucanase		<i>Thermophilic anaerobe NA10</i>	3.2.1.4	AB008029 BAA22939.1	O24820	
ORF TVG0696003		<i>Thermoplasma volcanium GSS1</i>	n.d.	AP000993 BAB59829.1 NC_002689 NP_111209.1	Q97AX2	
β -mannanase (ManB;TM1227)	Man5	<i>Thermotoga maritima</i>	3.2.1.78	AE001779 AAD36302.1 Y17980 CAB56854.1 NC_000853 NP_229032.1	Q9X0V4	
endoglucanase (TM1751)	Cel5A	<i>Thermotoga maritima</i>	3.2.1.4	AE001813 AAD36816.1 NC_000853 NP_229549.1	Q9X273	
ORF TM1752	Cel5B	<i>Thermotoga maritima</i>	n.d.	AE001813 AAD36817.1 NC_000853 NP_229550.1	Q9X274	
β -mannosidase		<i>Thermotoga neapolitana</i>	3.2.1.25	AY033477 AAK53459.1 Y17981 CAB56856.1		
cellulase		<i>Thermus caldophilus</i>	3.2.1.4	AF289822 AAK60011.1		
endo-1,6-glucanase		<i>Trichoderma harzianum</i>	3.2.1.75	X79197 CAA55789.1	Q12711 Q12712	
β -mannanase		<i>Trichoderma reesei (Hypocrea jecorina)</i>	3.2.1.78	L25310 AAA34208.1	Q99036	1QNO A 1QNP A 1QNQ A 1QNR A 1QNS A
endo-1,4-glucanase II	Cel5A	<i>Trichoderma reesei (Hypocrea jecorina)</i>	3.2.1.4	M19373 AAA34213.1	P07982	
endo-1,4-glucanase II		<i>Trichoderma viride</i>	3.2.1.4	AB021657 BAA36216.1	O93833	
endo-1,4-glucanase (Cel)		<i>Unidentified bacterium</i>	3.2.1.4	U12011 AAA91966.1	Q60054	
Sequence 1 from patent US 6190899		<i>Unknown</i>	n.d.	AAE60112.1		
Sequence 2 from patent US 6440911		<i>Unknown.</i>	n.d.	AAN27517.1		
Sequence 4 from patent US 6440911		<i>Unknown.</i>	n.d.	AAN27518.1		
β -mannanase		<i>Vibrio sp. MA-138</i>	3.2.1.78	D86329 BAA25188.1	O69347	
endoglucanase		<i>Volvariella volvacea V14</i>	3.2.1.4	AF329732 AAG59832.1		
endo-1,4-glucanase (ENG)		<i>Xanthomonas albilineans</i>	3.2.1.4	L26543 AAA27599.1	Q60100	
ORF Egl		<i>Xanthomonas axonopodis pv. citri str. 306</i>	n.d.	AE011625 AAM34920.1 NC_003919 NP_640384.1		
ORF Egl		<i>Xanthomonas axonopodis pv. citri str. 306</i>	n.d.	AE011626 AAM34921.1 NC_003919 NP_640385.1		

ORF Egl	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011626 AAM34922.1 NC_003919 NP_640386.1	
ORF EngXCA	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011689 AAM35501.1 NC_003919 NP_640965.1	
ORF XAC0346	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011660 AAM35238.1 NC_003919 NP_640702.1	
ORF XAC0933 (fragment)	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011724 AAM35821.1 NC_003919 NP_641285.1	
ORF XAC0934 (fragment)	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011724 AAM35822.1 NC_003919 NP_641286.1	
ORF XAC1796	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	n.d.	AE011812 AAM36659.1 NC_003919 NP_642123.1	
endo-1,4-glucanase	<i>Xanthomonas campestris</i>	3.2.1.4	M32700 AAA27612.1 AJ304415 CAC18529.1	P19487
EngXCA	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012472 AAM42791.1 NC_003902 NP_638867.1	
ORF Egl	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012095 AAM39345.1 NC_003902 NP_635421.1	
ORF Egl	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012096 AAM39346.1 NC_003902 NP_635422.1	
ORF Egl	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012096 AAM39347.1 NC_003902 NP_635423.1	
ORF XCC0857	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012185 AAM40172.1 NC_003902 NP_636248.1	
ORF XCC1778	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012279 AAM41068.1 NC_003902 NP_637144.1	
ORF XCC3535	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	n.d.	AE012474 AAM42805.1 NC_003902 NP_638881.1	
ORF XF0810	<i>Xylella fastidiosa</i> 9a5c	n.d.	AE003920 AAF83620.1 NC_002488 NP_298100.1	Q9PF68
ORF XF0818	<i>Xylella fastidiosa</i> 9a5c	n.d.	AE003921 AAF83628.1 NC_002488 NP_298108.1	Q9PF60
ORF XF2708	<i>Xylella fastidiosa</i> 9a5c	n.d.	AE004077 AAF85505.1 NC_002488 NP_299985.1	Q9PA12
Egl	<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012561 AAO29885.1 NC_004556 NP_780236.1	
EngXCA	<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012560 AAO29683.1 NC_004556 NP_780034.1	
EngXCA	<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012560 AAO29688.1 NC_004556 NP_780039.1	
exo-1,3-glucanase	<i>Yarrowia lipolytica</i>	3.2.1.58	Z46872 CAA86952.1	Q12725

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Introduction to Carbohydrate- Binding Module Families

Carbohydrate-
Binding
Modules

Last updated on
2003 Apr 1

Introduction

A **carbohydrate-binding module (CBM)** is defined as contiguous amino acid sequence within a carbohydrate-active enzyme with a discreet fold having **carbohydrate-binding activity**. A few exceptions are CBMs in cellulosomal scaffoldin proteins and rare instances of independent putative CBMs. The requirement of CBMs existing as modules within larger enzymes sets this class of carbohydrate-binding protein apart from other non-catalytic sugar binding proteins such as lectins and sugar transport proteins.

CBMs were previously classified as cellulose-binding domains (CBDs) based on the initial discovery of several modules that bound cellulose [1, 2]. However, additional modules in carbohydrate-active enzymes are continually being found that bind carbohydrates other than cellulose yet otherwise meet the CBM criteria, hence the need to reclassify these polypeptides using more inclusive terminology.

Family classification

Previous classification of cellulose-binding domains were based on amino acid similarity [3]. Groupings of CBDs were called "Types" and numbered with roman numerals (e.g. Type I or Type II CBDs). In keeping with the glycoside hydrolase classification, these groupings are now called families and numbered with Arabic numerals. Families 1 to 13 are the same as Types I to XIII [3].

The family classification of CBMs is expected to:

1. aid in the identification of CBMs
2. in some cases, predict binding specificity
3. aid in identifying functional residues
4. reveal evolutionary relationships
5. be predictive of polypeptide folds

14

This document provides an updated list of the CBM-containing proteins, arranged by CBM family. When a protein contains CBDs from **different** families, it appears in **each** appropriate family. Because the fold of proteins is better conserved than their sequences, some of the CBM families are likely to form **superfamilies** or **clans**.

References

1. Tomme, P. & Claeyssens, M. (1989) Identification of the functional important carboxylgroup in cellobiohydrolase I from *Trichoderma reesei* : a chemical modification study. FEBS Lett. 243, 239-243
2. Gilkes, N.R., Warren, R.A., Miller, R.C.J. & Kilburn, D.G. (1988) Precise excision of the cellulose binding domains from two *Cellulomonas fimi* cellulases by a homologous protease and the effect on catalysis. J.Biol.Chem. 263, 10401-10407
3. Tomme, P., Warren, R.A., Miller, R.C., Jr., Kilburn, D.G. & Gilkes, N.R. (1995) in Enzymatic Degradation of Insoluble Polysaccharides (Saddler, J.N. & Penner, M., eds.), Cellulose-binding domains: classification and properties. pp. 142-163, American Chemical Society, Washington

Note

The GenBank, SWISS-PROT, and/or PDB entries for these proteins are therefore mentioned in each of the relevant list of family members.

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Family CBM3

Family CBM3

CAZy Family Carbohydrate-Binding Module Family 3

Description Carbohydrate-binding module 3. Modules of approx. 150 residues found in bacterial enzymes. The cellulose-binding function has been demonstrated in many cases. In one instance binding to chitin has been reported.

3D Structure Status Available (see PDB). Fold β -sandwich

Note Previously known as cellulose-binding domain family III (CBD III).

Relevant Links HOMSTRAD; InterPro; PFAM

Statistics CAZy(62); GenBank/GenPept (71); Swissprot (45); PDB (10); 3D(4)

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
scaffoldin CipV	<i>Acetivibrio cellulolyticus</i>	n.d.	AF155197 AAF06064.1	Q9RPL0	
cellulase CelA	<i>Anaerocellum thermophilum</i>	3.2.1.91 3.2.1.4	Z86105 CAB06786.1	P96311	
endoglucanase A (EngA)	<i>Bacillus amyloliquefaciens</i> <i>UMAS1002</i>	n.d.	AF363635 AAL99668.1		
endo-1,4-glucanase 3a	<i>Bacillus lautus</i>	3.2.1.4	A28175 CAA01935.1		
ORF 1	<i>Bacillus lautus</i>	n.d.	M76588 AAA22302.1	P29718	
endoglucanase	<i>Bacillus pumilus</i> S-27	3.2.1.4	AF206716 AAF15367.1		
endo-1,4-glucanase	<i>Bacillus</i> sp. 5H	3.2.1.4	AB016164 BAA31712.1	O83012	
CelS	<i>Bacillus</i> sp. 79-23	3.2.1.4	AF045482 AAC02536.1	O52731	
endoglucanase CelB	<i>Bacillus</i> sp. BP23	3.2.1.4	AJ133614 CAB38941.1	Q9Z411	
endo-1,4-glucanase	<i>Bacillus</i> sp. D04	3.2.1.4	U27084 AAC43478.1	Q45430	
endo-1,4-glucanase IV	<i>Bacillus</i> sp. KSM-522	3.2.1.4	AB004098 BAA24918.1	O50589 P28622	
endo-1,4-glucanase	<i>Bacillus subtilis</i>	3.2.1.4	M28332 AAA22307.1	Q45532	
endo-1,4-glucanase	<i>Bacillus subtilis</i> BSE616	3.2.1.4	D01057 BAA00859.1	P23549	
endo-1,4- β -glucanase	<i>Bacillus subtilis</i> CHZ1	3.2.1.4	AY044252 AAK94871.1		
endo-1,4-glucanase	<i>Bacillus subtilis</i> DLG	3.2.1.4	M16185 AAA22496.1	P07983	
endo-1,4-glucanase (EglS or BglC)	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	3.2.1.4	AF355629 AAK39540.1 X04689 CAA28392.1 X67044 CAA47429.1 Z29076 CAA82317.1 Z73234 CAA97610.1 Z99113 CAB13696.1 NC_000964 NP_389695.1	P10475	
scaffoldin CipBc	<i>Bacteroides cellulosolvens</i>	none	AF224509 AAG01230.1	Q9FDJ9	
β -1,4-mannanase (ManA)	<i>Caldibacillus cellulosovorans</i>	3.2.1.78	AF163837 AAF22274.1	Q9RFX5	

ORF (fragment)		<i>Caldibacillus cellulovorans</i>	n.d.	AF200304 AAF61648.1	
ORF1 (fragment)		<i>Caldibacillus cellulovorans</i>	n.d.	AF163837 AAF22273.1	
xylanase XynA		<i>Caldibacillus cellulovorans</i>	3.2.1.8	AF200304 AAF61649.1	
β -mannanase/endo-1,4-glucanase		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.4 3.2.1.78	L01257 AAA71887.1	P22533
CelA		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.4	L32742 AAA91086.1	P22534
endo-1,4-glucanase/cellobiohydrolase		<i>Caldicellulosiruptor saccharolyticus</i>	3.2.1.91 3.2.1.4	X13602 CAA31936.1	P10474
xynC (multidomain protein)		<i>Caldicellulosiruptor sp. Rt69B.1</i>	3.2.1.8	AF036924 AAB95326.1	O52374
CelB (multidomain protein)		<i>Caldicellulosiruptor sp. Tok7B.1</i>	n.d.	AF078737 AAD30364.1	Q9X3P6
ORF5		<i>Caldicellulosiruptor sp. Tok7B.1</i>	n.d.	AF078038 AAK06388.1	
xylanase/arabinosidase XynA		<i>Caldicellulosiruptor sp. Tok7B.1</i>	3.2.1.8 3.2.1.55	AF078737 AAD30363.1	Q9X3P5
endo-1,4-glucanase B	<i>Cel9A</i>	<i>Cellulomonas fimi</i>	3.2.1.4	M64644 AAA23086.1	P26225
ORF CAC0910		<i>Clostridium acetobutylicum ATCC 824</i>	n.d.	AE007606 AAK78886.1	Q977Y4
ORF CAC0913		<i>Clostridium acetobutylicum ATCC 824</i>	n.d.	AE007607 AAK78889.1	Q97KK5
ORF CAC0916		<i>Clostridium acetobutylicum ATCC 824</i>	n.d.	AE007607 AAK78892.1	Q97KK3
cellulase H (CelH)	<i>Cel9H</i>	<i>Clostridium cellulolyticum</i>	3.2.1.4	AF316823 AAG45157.1	Q9EYQ5
cellulase J (CelJ)	<i>Cel9J</i>	<i>Clostridium cellulolyticum</i>	3.2.1.4	AF316823 AAG45158.1	Q9EYQ4
endo-1,4-glucanase G (CelCG)	<i>Cel9G</i>	<i>Clostridium cellulolyticum</i>	3.2.1.4	M87018 AAA73868.1	P37700 1G87 1GA2 1K72 1KFG 1G43 A
scaffoldin CipC		<i>Clostridium cellulolyticum</i>	none	U40345 AAC28899.1	Q45996
endo-1,4-glucanase H (fragment)		<i>Clostridium cellulovorans</i>	3.2.1.4	U34793 AAC38572.2	O65987
scaffoldin CbpA		<i>Clostridium cellulovorans</i>	none	M73817 AAA23218.1	P38058
scaffoldin CipA		<i>Clostridium josui</i>	none	AB004845 BAA32429.1	
cellobiohydrolase Y (avicelase II) (CelY)		<i>Clostridium stercoararium</i>	3.2.1.91	Z69359 CAA93280.1	P50900
endo-1,4-glucanase Z (avicelase I) (CelZ)		<i>Clostridium stercoararium</i>	3.2.1.4	X55299 CAA39010.1	P23659
endoglucanase Q (CelQ)	<i>Cel9I</i>	<i>Clostridium thermocellum</i>	3.2.1.4	AB047845 BAB33148.1	
scaffoldin CipA		<i>Clostridium thermocellum ATCC 27405</i>	none		Q06851 1NBC A
ORFZ		<i>Clostridium thermocellum DSM 1237</i>	n.d.	Z68924 CAA93151.2 AJ420770 CAD12660.1	Q46392
1,4- β -cellobiohydrolase (CelO)		<i>Clostridium thermocellum F7</i>	3.2.1.91	AJ275975 CAB76938.1	
cellobiohydrolase A (CbhA)		<i>Clostridium thermocellum F7</i>	3.2.1.91	X80993 CAA56918.1	Q59325
endo-1,4-glucanase (CelN)		<i>Clostridium thermocellum F7</i>	3.2.1.4	AJ275974 CAB76935.1	

endo-1,4-glucanase F	Cel9B	<i>Clostridium thermocellum</i>	3.2.1.4	X60545 CAA43035.1	P26224	
		NCIB 10682				
endo-1,4-glucanase I (Cell or CMC)	Cel9C	<i>Clostridium thermocellum</i>	3.2.1.4	L04735 AAA20892.1	Q02934	
		NCIB10682 / F7		AJ275974 CAB76932.1		
endo-1,4-glucanase N		<i>Erwinia carotovora</i>	3.2.1.4	L39788 AAC37033.1	Q59394	
		atroseptica				
endo-1,4-glucanase V1		<i>Erwinia carotovora</i>	3.2.1.4	X79241 CAA55823.1	Q59395	
		SCC3193				
endo-1,4-glucanase V		<i>Erwinia carotovora</i>	3.2.1.4	X76000 CAA53592.1	Q47096	
		SCRI193				
endo-1,4-glucanase CelA (fragment)		<i>Erwinia carotovora</i>	3.2.1.4	AF025768 AAC02964.1	O31029	
		subsp. carotovora LY34				
cellulose-binding protein E1 (Cbpe1)		<i>Eubacterium</i>	n.d.	AB072270 BAB86305.1		
		cellulosolvens				
endo-1,4-glucanase A		<i>Paenibacillus lautus</i>	3.2.1.4	M76588 AAA22303.1	P29719	
cellobiohydrolase Cel48C	Cel48C	<i>Paenibacillus</i> sp. BP-23	3.2.1.91	AJ488933 CAD32945.1		
cellulase VI (Cel9A)	Cel9A	<i>Ruminococcus albus</i> F-40	n.d.	AB028321 BAB64431.1		
ORF SCF11.15		<i>Streptomyces coelicolor</i>	n.d.	AL132662 CAB59592.1		
		A3(2)		NC_003888 NP_624849.1		
endo/exo-1,4-glucanase E4	Cel9A	<i>Thermobifida fusca</i>	3.2.1.4	L20093 AAB42155.1	P26221	1JS4 A
			3.2.1.91		Q08167	1TF4 A
						3TF4 A
						4TF4 A
endo-1,4-glucanase		<i>Thermophilic anaerobe</i>	3.2.1.4	AB008029 BAA22939.1	O24820	
		NA10				
Sequence from patent		Unknown	none	- AAE16382.1		
				- AAO30719.1		
Sequence 10 from patent US 6429000		Unknown.	n.d.	AAN26180.1		

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Family CBM2

Family CBM2

CAZy Family Carbohydrate-Binding Module Family 2

Description Carbohydrate-binding module 2. Modules of approx. 100 residues and which are found in a large number of bacterial enzymes. The cellulose-binding function has been demonstrated in many cases. Several of these modules have been shown to also bind chitin or xylan.

3D Structure Status Available (see PDB)

Note Previously known as cellulose-binding domain family II (CBD II).

Relevant Links HOMSTRAD; InterPro; PFAM

Statistics CAZy(107); GenBank/GenPept (143); Swissprot (83); PDB (10); 3D(11)

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
endo-1,4-glucanase	<i>Acidothermus cellulolyticus</i>	3.2.1.4	U33212 AAA75477.1 AX467594 CAD42489.1	P54583	3D
endo-1,4-glucanase	<i>Actinomyces</i> sp. 40	3.2.1.4	U94825 AAC06196.1	O66064	
ORF PCZA361.11 (putative oxidoreductase)	<i>Amycolatopsis orientalis</i>	n.d.	AJ223998 CAA11769.1	O52799	
ORF egl	<i>Azorhizobium caulinodans</i> ORS571	n.d.	Z48958 -		
BA_0961	<i>Bacillus anthracis</i> str. A2012	n.d.	NC_003995 NP_654321.1		
chitinase CW (ChiCW)	<i>Bacillus cereus</i> 28-9	3.2.1.14	AF416570 AAM48520.1		
chitinase B	<i>Bacillus cereus</i> CH	3.2.1.14	AB041932 BAB16891.1	Q9FAC8	
chitinase	<i>Bacillus thuringiensis</i>	3.2.1.14	U89796 AAB58579.1	O07088	
chitinase (Chi)	<i>Bacillus thuringiensis</i>	3.2.1.14	AF424979 AAL17867.1 AY074882 AAL71886.2		
chitinase	<i>Bacillus thuringiensis</i> serovar <i>israelensis</i>	n.d.	AF526379 AAM88400.1		
chitinase (Kchi)	<i>Bacillus thuringiensis</i> serovar <i>kurstaki</i>	n.d.	AY189740 AAO34713.1		
chitinase	<i>Bacillus thuringiensis</i> serovar <i>sofio</i>	n.d.	AY129671 AAM94024.1		
endo-1,4-glucanase 1	<i>Butyrivibrio fibrisolvens</i> H17c	3.2.1.4	- AAE29745 X17538 CAA35574.1	P20847	
cellobiohydrolase A	Cel6B <i>Cellulomonas fimi</i>	3.2.1.91	L25809 AAC36898.1	P50401	
cellobiohydrolase B	Cel48A <i>Cellulomonas fimi</i>	3.2.1.91	L38827 AAB00822.1	P50899	
endo-1,4-glucanase A	Cel6A <i>Cellulomonas fimi</i>	3.2.1.4	M15823 AAA23084.1	P07984	
endo-1,4-glucanase B	Cel9A <i>Cellulomonas fimi</i>	3.2.1.4	M64644 AAA23086.1	P26225	
endo-1,4-glucanase D	Cel5A <i>Cellulomonas fimi</i>	3.2.1.4	L02544 AAA23089.1	P50400	
xylanase (Cex)	Xyn10A <i>Cellulomonas fimi</i>	3.2.1.8	M15824 AAA56791.1 L11080 AAA56792.1	P07986 Q59277	1EXG 1EXH
xylanase D	Xyn11A <i>Cellulomonas fimi</i>	3.2.1.8	X76729 CAA54145.1	P54865	1E5B A

			3.1.1.72			1E5C A 1HEH C 1HEJ C 1XBD _ 2XBD _
endo-1,4-glucanase B (cfIB)	<i>Cellulomonas flavigena</i>		3.2.1.4	AF172345 AAD48494.2		
xylanase (fragment)	<i>Cellulomonas flavigena</i> CDBB5321		3.2.1.8	AF338352 AAK15536.1	Q9AG99	
xylanase	<i>Xyn11A Cellulomonas pachnodae</i>		3.2.1.8	AF120156 AAD54767.1	Q9RQB8	
chitinase 63 (Chi63)	<i>Cellulomonas sp. GM13</i>		3.2.1.14	AF181718 AAF00931.2		
endo-b1,4-mannanase 5B	<i>Man5B Cellvibrio japonicus</i>		n.d.	AY187032 AAO31760.1		
arabinofuranosidase C	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		3.2.1.55	X54523 CAA38390.1	P23031	
cellodextrinase C	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		3.2.1.-	X61299 CAA43597.1	P27033	
endo-1,4-glucanase A	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		3.2.1.4	X12570 CAA31082.1	P10476	
endo-1,4-glucanase B	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		3.2.1.4	X52615 CAA36844.1	P18126	
endo-1,4-glucanase E	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		3.2.1.4	X86798 CAA60493.1	Q59665	
esterase D	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		n.d.	X58956 CAA41727.1	Q51815	
pectate lyase (PelA)	<i>Pel10A Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		4.2.2.2	AF279264 AAG29353.1	Q9F7L3	3D
rhamnogalacturonan lyase	<i>Rgl11A Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		4.2.2.-	AY026755 AAK20911.1	Q9AF09	
xylanase A	<i>Xyn10A Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		3.2.1.8	X15429 CAA33469.1	P14768	3D
xylanase B	<i>Cellvibrio japonicus</i> (formerly <i>Pseudomonas cellulosa</i>)		3.2.1.8	X54523 CAA38389.1	P23030	
chitinase vChti-1	<i>Chlorella virus CVK2</i>		3.2.1.14	AB022343 BAA78554.1	Q9WAX4	
Cellulase CelA	<i>Clavibacter michiganensis</i> NCPB 382		3.2.1.4	X62582 CAA44467.2	Q9K5C7	
cellulase CelA	<i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i>		3.2.1.4	AY007311 AAK16222.1	Q9AF65	
endo-1,4-glucanase D	<i>Clostridium cellulovorans</i>		3.2.1.4	M37434 AAA23233.1	P28623	
endo-1,4-glucanase (CelA)	<i>Clostridium longisporum</i>		3.2.1.4	L02868 AAC37035.1	P54937	
CMC-xylanase (fragment)	<i>Fibrobacter succinogenes</i> S85		3.2.1.4 3.2.1.8	U94826 AAC06197.1	O66065	
endoglucanase 1 (Eng1)	<i>Globodera rostochiensis</i>		3.2.1.4	AF004523 AAC48325.1 AF056110 AAC63988.1	O16028	
endoglucanase 1 (Eng1)	<i>Heterodera glycines</i>		3.2.1.4	AF052733 AAC15707.1 AF006052 AAC48327.1 A79341 CAB59144.1	O18453	
β -1,4-endoglucanase Eng-1a	<i>Meloidogyne incognita</i>		3.2.1.4	AF323087 AAK21882.1	Q9BJZ1	
cellulose -binding protein	<i>Meloidogyne incognita</i>		none	AF049139 AAC05133.1	O61530	

endo-1,4-glucanase 1 (Eng-1)	<i>Meloidogyne incognita</i>	3.2.1.4	AF100549 AAD45868.1	Q9UA57
ORF X (fragment)	<i>Methylococcus capsulatus</i> <i>Bath</i>	n.d.	AF447860 AAL40976.1	
endo-1,4-glucanase A	<i>Microbispora bispora</i>	3.2.1.4		P26414
endo-1,4-glucanase	<i>Micromonospora</i> <i>cellulolyticum</i>	3.2.1.4	S76408 AAC60491.1	Q53488
ORF MT2041	<i>Mycobacterium tuberculosis</i> <i>CDC1551</i>	n.d.	AE007056 AAK46316.1 NC_002755 NP_336502.1	
ORF Rv1987	<i>Mycobacterium tuberculosis</i> <i>H37Rv</i>	n.d.	Z74025 CAA98397.1 NC_000962 NP_216503.1	Q10870
endoxylanase (XynA)	<i>Nonomuraea flexuosa</i>	3.2.1.8	AJ508952 CAD48747.1	
ORF A181/182R	<i>Paramecium bursaria</i> <i>Chlorella virus 1</i>	3.2.1.14	U42580 AAC96549.2 NC_000852 NP_048529.1	Q84501 Q84502
ORF PF1233	<i>Pyrococcus furiosus</i> DSM 3638	n.d.	AE010230 AAL81357.1 NC_003413 NP_578962.1	Q8U1H5
ORF RSp0583	<i>Ralstonia solanacearum</i> <i>GMI1000</i>	n.d.	AL646079 CAD17734.1 NC_003296 NP_522144.1	Q8XS97
chitinase C (2SC6G5.20c)	<i>Streptomyces coelicolor</i> A3 (2)	3.2.1.14	AB017010 BAA75644.1 AL359152 CAB94547.1 NC_003888 NP_629515.1	Q9Z9M8
ORF 2SCC13.07c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL442165 CAC10108.1 NC_003888 NP_627029.1	Q9F3I2
ORF AxeA	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL133220 CAB61737.1 NC_003888 NP_626539.1	Q9RKN7
ORF CelB (SCG11A.18)	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL133210 CAB61599.1 NC_003888 NP_625477.1	Q9RJY3
ORF CelS2 (SCG11A.19)	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL133210 CAB61600.1 NC_003888 NP_625478.1	Q9RJY2
ORF SC10F4.10c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL450350 CAC16970.1 NC_003888 NP_631677.1	Q9F3Q0
ORF SC4H2.07c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL022268 CAA18323.1 NC_003888 NP_629910.1	O69962
ORF SC5C7.30c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL031515 CAA20642.1 NC_003888 NP_630626.1	O86727
ORF SC5C7.31c	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL031515 CAA20643.1 NC_003888 NP_630627.1	O86728
ORF SC5C7.33	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL031515 CAA20645.1 NC_003888 NP_630629.1	O86730
ORF SC7H1.24	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL021411 CAA16211.1 NC_003888 NP_630071.1	O54183
ORF SCF11.34c (ManA)	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL132662 CAB59611.1 AL939106 CAD55266.1	
ORF SCF91.34c (XlnA)	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL132973 CAB61191.1 NC_003888 NP_624983.1	Q9RJ91
ORF XlnB	<i>Streptomyces coelicolor</i> A3 (2)	n.d.	AL133220 CAB61738.1 NC_003888 NP_626540.1	Q9RKN6
chitinase III (Chi III) (fragment)	<i>Streptomyces griseus</i> HUT 6037	3.2.1.14	AB081807 BAB86377.1	
cellulose binding protein (ORF2)	<i>Streptomyces halstedii</i>	n.d.	U51222 AAC45430.1	O07862
endo-1,4-glucanase	<i>Streptomyces halstedii</i>	3.2.1.4	U51222 AAC45429.1	O08468
xylanase	<i>Streptomyces halstedii</i> JMB	3.2.1.8	U41627 AAC45554.1	Q59922 1NQ6
acetyl xylan esterase	<i>Streptomyces lividans</i>	3.1.1.72	M64552 AAC06115.2	Q54413
chitinase C	<i>Streptomyces lividans</i>	3.2.1.14	D12647 BAA02168.1	P36909
endo-1,4-glucanase	<i>Streptomyces lividans</i>	3.2.1.4	M82807 -	P27035
endo-1,4-glucanase	<i>Streptomyces lividans</i>	3.2.1.4	U04629 AAB71950.1	Q54331 3D
xylanase B	<i>Streptomyces lividans</i>	3.2.1.8	M64552 AAC06114.2	P26515
chitinase C	<i>Streptomyces peucetius</i>	3.2.1.14	AF206633 AAF43629.1	Q9L8G0
chitinase-63	<i>Streptomyces plicatus</i>	3.2.1.14	M18397 AAA26717.1	P11220

21

endo-1,4-glucanase S		<i>Streptomyces rochei</i> A2	3.2.1.4	M82804 AAA26720.1	
cellulase 12A	<i>Cel12A</i>	<i>Streptomyces sp.</i> 11AG8	3.2.1.4	X73953 CAA52139.1	Q59963
				AF233376 AAE59731.1	Q9KIH1 10A4
				AAF91283.1	
xylanase B		<i>Streptomyces thermocyaneoviolaceus</i>	3.2.1.8	AF194025 AAF04601.1	Q9RMM4
acetyl xylan esterase STX-III		<i>Streptomyces thermoviolaceus</i>	3.1.1.6	D85898 BAA19779.1	O08347
			3.1.1.72		
xylanase II		<i>Streptomyces thermoviolaceus</i>	3.2.1.8	D85897 BAA19778.1	O08346
chitin-binding protein celS2		<i>Streptomyces viridosporus</i>	none	AF126376 AAD27623.1	Q9X5K8
endo-1,4-glucanase S1		<i>Streptomyces viridosporus</i>	3.2.1.4	AF130408 AAD25090.1	
xylanase (SvxA)		<i>Streptomyces viridosporus</i>	3.2.1.8	AF198618 AAF09501.1	
ORF slr0897		<i>Synechocystis sp.</i> PCC 6803	n.d.	D64003 BAA10447.1	Q55365
				NC_000911.1 NP_442377.1	
cellobiohydrolase E3	<i>Cel6B</i>	<i>Thermobifida fusca</i>	3.2.1.91	U18978 AAA62211.1	Q60029
endo-1,4-glucanase E1	<i>Cel9B</i>	<i>Thermobifida fusca</i>	3.2.1.4	L20094 AAC06387.1	Q08166
endo-1,4-glucanase E2	<i>Cel6A</i>	<i>Thermobifida fusca</i>	3.2.1.4	M73321 AAC06388.1	P26222 3D
endo-1,4-glucanase E5	<i>Cel5A</i>	<i>Thermobifida fusca</i>	3.2.1.4	L01577 AAC09379.1	Q01786
endo/exo-1,4-glucanase E4	<i>Cel9A</i>	<i>Thermobifida fusca</i>	3.2.1.4	L20093 AAB42155.1	P26221 3D
			3.2.1.91		Q08167
exocellulase E6 (CelF)	<i>Cel48A</i>	<i>Thermobifida fusca</i>	3.2.1.91	AF144563 AAD39947.1	
xylanase		<i>Thermobifida fusca</i>	3.2.1.8	U01242 AAA21480.1	Q56265
chitinase A		<i>Thermococcus kodakaraensis</i>	3.2.1.14	T43916	
xylanase		<i>Thermomonospora alba</i>	3.2.1.8	Z81013 CAB02654.1	P74912
unnamed protein product		unidentified	n.d.	AX565635 CAD58415.1	
Sequence 2 from patent US 6207436		Unknown.	n.d.	AAE63612.1	
ORF EngXCA		<i>Xanthomonas axonopodis</i> pv. citri str. 306	n.d.	AE011689 AAM35501.1	
				NC_003919 NP_640965.1	
endo-1,4-glucanase		<i>Xanthomonas campestris</i>	3.2.1.4	M32700 AAA27612.1	P19487
				AJ304415 CAC18529.1	
EngXCA		<i>Xanthomonas campestris</i> pv. campestris str. ATCC 33913	n.d.	AE012472 AAM42791.1	
				NC_003902 NP_638867.1	
ORF XF0818		<i>Xylella fastidiosa</i> 9a5c	n.d.	AE003921 AAF83628.1	Q9PF60
				NC_002488 NP_298108.1	
ORF XF1267		<i>Xylella fastidiosa</i> 9a5c	n.d.	AE003960 AAF84076.1	Q9PDW2
				NC_002488 NP_298556.1	
EngXCA		<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012560 AAO29683.1	
				NC_004556 NP_780034.1	
GuxA		<i>Xylella fastidiosa</i> Temecula1	n.d.	AE012555 AAO28402.1	
				NC_004556 NP_778753.1	

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22

CAZy - Carbohydrate-Active enZYmes

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2. Quote papers where CAZy(ModO) is revealed:

Coutinho, P.M. & Henrissat, B. (1999) Carbohydrate-active enzymes: an integrated database approach. In *"Recent Advances in Carbohydrate Bioengineering"*, H.J. Gilbert, G. Davies, B. Henrissat and B. Svensson eds., The Royal Society of Chemistry, Cambridge, pp. 3-12.

Coutinho, P.M. & Henrissat, B. (1999) The modular structure of cellulases and other carbohydrate-active enzymes: an integrated database approach. In *"Genetics, Biochemistry and Ecology of Cellulose Degradation"*, K. Ohmiya, K. Hayashi, K. Sakka, Y. Kobayashi, S. Karita and T. Kimura eds., Uni Publishers Co., Tokyo, pp. 15-23.

3. Quote the references concerning the family classification(s) in question:

Glycosidases and Transglycosidases (or Glycoside Hydrolases)


Glycosyltransferases

Polysaccharide Lyases (*cite CAZyModO*)

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ID MANB_CALSA STANDARD; PRT; 1331 AA.
 AC P22533;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Beta-mannanase/endoglucanase A precursor [Includes: Mannan endo-1,4-
 DE beta-mannosidase A (EC 3.2.1.78) (Beta-mannanase) (Endo-1,4-
 DE mannanase); Endo-1,4-beta-glucanase (EC 3.2.1.4) (Cellulase)].
 GN MANA.
 OS *Caldocellum saccharolyticum* (*Caldicellulosiruptor saccharolyticus*).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
 OC *Caldicellulosiruptor*.
 OX NCBI_TaxID=44001;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93119139; PubMed=1476429; [NCBI, ExPASy, EBI, Israel, Japan]
 RA Gibbs M.D., Saul D.J., Luthi E., Bergquist P.L.;
 RT "The beta-mannanase from '*Caldocellum saccharolyticum*' is part of a
 RT multidomain enzyme.";
 RL Appl. Environ. Microbiol. 58:3864-3867(1992).
 RN [2]
 RP SEQUENCE OF 1-346 FROM N.A.
 RX MEDLINE=91247819; PubMed=2039230; [NCBI, ExPASy, EBI, Israel, Japan]
 RA Luethi E., Jasmat N.B., Grayling R.A., Love D.R., Bergquist P.L.;
 RT "Cloning, sequence analysis, and expression in *Escherichia coli* of a
 RT gene coding for a beta-mannanase from the extremely thermophilic
 RT bacterium '*Caldocellum saccharolyticum*'.";
 RL Appl. Environ. Microbiol. 57:694-700(1991).
 CC -!- FUNCTION: DEGRADATION OF HEMICELLULOSES, THE SECOND MOST ABUNDANT
 CC POLYSACCHARIDES IN NATURE. CONTAINS TWO CATALYTIC DOMAINS WITH
 CC MANNANASE AND ENDOGLUCANASE ACTIVITIES.
 CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic
 CC linkages in mannans, galactomannans, glucomannans, and
 CC galactoglucomannans.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -!- MISCELLANEOUS: THIS ENZYME IS MOST ACTIVE AT PH 6 AND 80 DEGREES
 CC CELSIUS.
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
 CC A (FAMILY 5 OF GLYCOSYL HYDROLASES).
 CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
 CC J (FAMILY 44 OF GLYCOSYL HYDROLASES).
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DR EMBL; L01257; AAA71887.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 DR EMBL; M36063; AAA72861.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 DR PIR; B43745; B43745.
 DR PIR; A48954; A48954.
 DR HSSP; Q06851; 1NBC. [HSSP ENTRY / SWISS-3DIMAGE / PDB]
 DR InterPro; IPR001956; CBD 3.
 DR InterPro; IPR001547; Glyco hydro 5.
 DR InterPro; Graphical view of domain structure.
 DR Pfam; PF00150; cellulase; 1.
 DR Pfam; PF00942; CBM 3; 2.
 DR ProDom; PD001947; CBD 3; 2.
 DR ProDom [Domain structure / List of seq. sharing at least 1 domain]
 DR PROSITE; PS00659; GLYCOSYL HYDROL F5; 1.
 DR BLOCKS; P22533.
 DR ProtoNet; P22533.
 DR ProtoMap; P22533.
 DR PRESAGE; P22533.
 DR DIP; P22533.
 DR ModBase; P22533.
 DR SWISS-2DPAGE; GET REGION ON 2D PAGE.
 KW Hydrolase; Glycosidase; Cellulose degradation; Signal;
 KW Multifunctional enzyme.
 FT SIGNAL 1 41 POTENTIAL.
 FT CHAIN 42 1331 BETA-MANNANASE/ENDOGLUCANASE A.
 FT DOMAIN 42 325 CATALYTIC (MANNANASE ACTIVITY). *GH5*
 FT DOMAIN 326 361 PRO/SER/THR-RICH (PT BOX).
 FT DOMAIN 362 518 *=156* SUBSTRATE-BINDING (POTENTIAL). *CBD II*
 FT DOMAIN 519 564 PRO/SER/THR-RICH (PT BOX).
 FT DOMAIN 565 720 *=155* SUBSTRATE-BINDING (POTENTIAL). *CBD II*
 FT DOMAIN 721 780 PRO/SER/THR-RICH (PT BOX).
 FT DOMAIN 781 1331 CATALYTIC (ENDOGLUCANASE ACTIVITY).
 FT ACT_SITE 162 162 PROTON DONOR (BY SIMILARITY).
 FT ACT_SITE 257 257 NUCLEOPHILE (BY SIMILARITY).
 FT CONFLICT 338 338 T -> P (IN REF. 2).
 FT CONFLICT 340 346 TPTPTPT -> RQHQRQ (IN REF. 2).
 SQ SEQUENCE 1331 AA; 146892 MW; FFBCA51BB8D8F0E0 CRC64;
 MRLKTKIRKK WLSVLCTVVF LLNILFIANV TILPKVGAAT SNDGVVKIDT STLIGTNHAH
 CWYRDRDLTA LRGISRSGMN SVRVVLSNGY RWTKIPASEV ANIISLSRSL GFKAIILEVH
 DTTGYGEDGA ACSLAQAVEY WKEIKSVLDG NEDFVIINIG NEPYGNNNYQ NWVNDTKNAI
 KALRDAGFKH TIMVDAPNWG QDWSNTMRDN AQSIMEADPL RNLVFSIHMY GVYNTASKVE
 EYIKSFVDKG LPLVIGFEGH QHTDGDPEDE AIVRYAKQYK IGLFSWSWCG NSSYVGYLDM
 VNNWDPNNPT PWGQWYKTNA IGTSSTPTPT STVTPTPTPT PTPTPTVTAT PTPTPTPVST
 PATSGQIKVL YANKETNSTT NTIRPWLKVV NSGSSSIDLS RVTIRYWYTV DGERAQSAIS
 DWAQIGASNV TFKFVKLSSS VSGADYYLEI GFKSGAGQLQ PGKDTGEIQM RFNKDDWSNY
 NQGNDWSWIQ SMTSYGENEK VTAYIDGVLV WGQEPGATP APAPTATPTP TPTVTPTPTV
 TPTPTVTATP TPTPTPTPTP VSTPATGGQI KVLANKETN STTNTIRPWL KVVNSGSSSI
 DLSRVITIRYW YTV DGERAQS AISDWAQIGA SNVTFKFVKL SSSVSGADYY LEIGFKSGAG
 QLQPGKDTGE IQIRFNKSDW SNYNQGNDSW WIQSMTSYGE NEKVYAYIDG VLVWGQEPG
 TTPSPTSTPT VVTPTPTPTPT PTPTPTPTPT PTPTVTPTPT VTATPTPTPT PIPTVTPLPT
 ISPPSPVVEI TINTNAGRTQ ISPYIYGANQ DIEGVVHSAR RLGGNRLTGY NWENNFSNAG
 NDWYHSSDDY LCWSMGISSG DAKVPAAVVS KFHEYSLKNN AYSATVLTQMA GYVSKDNYGT
 VSENETAPSN RWAIEVKFKKD APLSLNPDLN DNFVYMDEFI NYLINKYGMA SSPTGIKGYI
 LDNEPDLWAS THPRIHPNKV TCKELIEKSV ELAKVIKTLT PSAEVFGYAS YGFMGYYSLO
 DAPDWNQVKG EHRWFISWYL EQMKKASDSF GKRLLDVLDL HWYPEARGGN IRVCFDGENP
 TSKEVVIARM QAPRTLWDPT YKTSVKGQIT AGENSWINQW FSDYLPPIPN VKADIEKYYP
 GTKLAISEFD YGGRNHISGG IALADVGLIF GKYGVNFAAR WGDGSGYAAA AYNIIYLNLYDG

KGSKYGNTNV SANTSDVENM PVYASINGQD DSELHIILIN RNYDQKLQVK INITSTPKYT
KAIIYGFDSN SPEYKMGNI DNIESNVFTL EVPKFNGVSH SITLDFNVI KIIQNEVIKF
IRNLVFMRAL V

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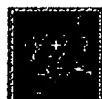
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